(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification[7]: G01N 33/68, C12Q 1/68, C07K 1/13

(21) International Application Number: PCT/GB03/01485

(22) International Filing Date: 4 April 2003 (04.04.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
02252440.9   4 April 2002 (04.04.2002)   EP

(71) Applicant (for all designated States except US): XZIL-LION GMBH & CO. KG [GB/DE]; Industriepark Hochst, Building G865, 65926 Frankfurt am Main (DE).

(72) Inventors; and
(75) Inventors/Applicants (for US only): THOMPSON, Andrew, Hugin [GB/GB]; 30 Canterbury Street, Cambridge CB4 3QF (GB). HAMON, Christian [FR/DE]; Luthmerstrasse 49, 65934 Frankfurt am Main (DE). KUHN, Karsten [DE/DE]; Querstrasse 29, 44139 Dortmund (DE). MEYER, Markus [DE/DE]; Buhlstrasse 26A, 37073 Gottingen (DE). JUERGEN, Schafer [DE/DE]; Am Langen Weg 2, 36341 Lauterbach (DE). NEUMANN, Thomas [DE/DE]; Loreleistrasse 26, 65929 Frankfurt am Main (DE).

(74) Agents: HILL, Christopher, Michael et al.; Page White & Farrer, 54 Doughty Street, London WC1N 2LS (GB).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
—   with international search report
—   before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHOD FOR CHARACTERISING ANALYTES

(57) Abstract: Provided is a method for characterising an analyte by matrix assisted laser desorption ionisation (MALDI) mass spectrometry, which method comprises: (a) labelling the analyte with a light-absorbing label that absorbs light at a pre-determined frequency, to form a labelled analyte; (b) embedding the labelled analyte in a matrix formed from at least one compound that absorbs light, to form an embedded labelled analyte; (c) desorbing the embedded labelled analyte by exposing it to light having the pre-determined frequency, to form a desorbed analyte; and (d) detecting the desorbed analyte by mass spectrometry to characterise the analyte.

METHOD FOR CHARACTERISING ANALYTES

This invention relates to methods of labelling analyte molecules, particularly non-volatile biomolecules, with markers that enhance the sensitivity with which their associated analyte biomolecule is detectable by Matrix Assisted Laser Desorption Ionisation (MALDI) Mass Spectrometry. Specifically this invention relates to the ability of certain dyes to improve the sensitivity of detection by MALDI mass spectrometry of analytes libelled with these dyes.

The identification of proteins in biological samples is an essential activity of biochemical analysis, particularly the determination of the sequence of a protein, since the sequence determines the structure of a protein, which, in turn, determines the function of the protein. Traditional techniques for protein identification are cumbersome and relatively slow. The mainstay of protein identification techniques has been chemical sequencing of peptides using the Edman degradation, which can sequentially identify amino acids in a peptide from the N-terminus. This sequencing technique is typically used in conjunction with enzymatic digestion of a protein or polypeptide. Typically, an unidentified polypeptide is digested and its component peptides are separated from each other by chromatography. The individual peptides are then subjected to Edman degradation. The sequences of the peptides can be ordered by comparing the sequences of peptides from digestion of the polypeptide with different sequence specific cleavage reagents. This process allows the complete sequence of a polypeptide to be determined. While this has been a highly successful technique for the identification of proteins, it is quite laborious. New technologies have made rapid protein identification more feasible such as Matrix Assisted Laser Desorption Ionisation Time-of-Flight (MALDI-TOF) mass spectrometry, which has permitted the development of peptide mass fingerprinting as a relatively rapid procedure for protein identification.

A typical peptide mass fingerprinting protocol involves determining the mass of the unidentified protein followed by digestion of the protein (in gel or in solution) with enzymes such as trypsin. Trypsin cleaves polypeptides selectively at arginine and lysine

residues, leaving either arginine or lysine at the C-termini of the product peptides. The positions of lysine and arginine in the sequence of a polypeptide determine where the polypeptide is cut giving rise to a characteristic series of peptides. The pattern of peptides can be easily detected by MALDI-TOF mass spectrometry. This mass spectrometric technique has a large mass range, can readily ionise large biomolecules, will preferentially produce singly charged ions and competition for ionisation with this technique is not severe, although competition can be problematic. This means that there is generally one peak in the mass spectrum for each peptide, the mass-to-charge ratio for each peak has essentially the same value as the mass of the peptide, with an added proton to ionise the peptide, and most (and sometimes all) the peptides from the tryptic digest of an unidentified protein can be analysed simultaneously. In effect the mass spectrum is a 'bar-code' in which the lines in the spectrum represent the masses of the characteristic cleavage peptides of the protein. For any given protein, there may be some peptides, which have the same mass as a peptide from another protein but it is very unlikely that two different proteins will give rise to peptides that all have identical masses. This means that the pattern of masses of the tryptic digest of a protein is a fairly unique identifier of that protein and is called a Peptide Mass Fingerprint (PMF). The relative uniqueness of PMFs means that databases of calculated (or theoretical) PMFs, determined from known protein sequences or sequences that have been predicted from genomic DNA or expressed sequence tags (ESTs), can be used to identify proteins in biological samples (Pappin DJC, Höjrup P and Bleasby AJ, Current Biology 3: 327-332, "Rapid identification of proteins by peptide-mass fingerprinting." 1993; Mann M, Hojrup P, Roepstorff P, Biol Mass Spectrom 22(6): 338-345, "Use of mass spectrometric molecular weight information to identify proteins in sequence databases." 1993; Yates JR 3rd, Speicher S, Griffin PR, Hunkapiller T, Anal Biochem 214(2): 397-408, "Peptide mass maps: a highly informative approach to protein identification." 1993). The PMF for an unidentified protein can be compared with all of the PMFs in a database to find the best match, thereby identifying the protein. Searches of this kind can be constrained by determining the mass of the protein prior to digestion. In this way the pattern of masses of an unidentified polypeptide can be related to its sequence, which in turn can help to determine the role of a protein in a particular sample.

There are, however, many technical difficulties involved in determining the PMF for a protein. A typical protein will give rise to twenty to thirty peptides after cleavage with trypsin, but not all of these peptides will appear in the mass spectrum. The precise reasons for this are not fully understood. One factor that is believed to cause incomplete spectra is competition for protonation during the ionisation process, resulting in preferential ionisation of arginine containing peptides (Krause E. & Wenschuh H. & Jungblut P.R., Anal Chem 71(19): 4160-4165, "The dominance of arginine-containing peptides in MALDI-derived tryptic mass fingerprints of proteins." 1999). In addition, there are surface effects that result from the process of preparing MALDI targets. The targets are prepared by dissolving the peptide digest in a solution of the matrix material. Small droplets of the peptide/matrix solution are dropped onto a metal target and left to dry. Differences in solubility of peptides will mean that some peptides will preferentially crystallise near the top surface of the matrix where they will be desorbed more readily.

Sensitivity is also a problem with conventional protocols for identifying proteins from their PMF. To be an effective tool, it should be possible to determine a PMF for as small a sample of protein as possible to improve the sensitivity of the analysis of protein samples.

Some attempts have been made to improve the ionisation of peptides that do not contain arginine by chemical derivatisation of peptides. Conversion of lysine to homo-arginine is one approach that has met with some success (V. Bonetto et al., Journal of Protein Chemistry 16(5): 371 – 374, "C-terminal Sequence Determination of Modified Peptides by MALDI MS", 1997; Francesco L. Brancia, Stephen G. Oliver and Simon J. Gaskell, Rapid Commun. in Mass Spec., 14, 2070-2073, "Improved matrix-assisted laser desorption/ionisation mass spectrometric analysis of tryptic hydrolysates of proteins following guanidination of lysine-containing peptides." 2000; Brancia et al., Electrophoresis 22: 552 – 559, "A combination of chemical derivatisation and improved bioinformatics tools optimises protein identification for proteomics", 2001). The conversion of lysine to homo-arginine introduces guanidino functionalities into all of the

peptides from a tryptic digest, with the exception of C-terminal peptides, greatly improving the representation of lysine containing peptides in the MALDI-TOF mass spectra.

The derivatisation of peptides to introduce guanidino-groups is a method of improving the proton affinity of the derivatised peptide. This approach to improve sensitivity has been moderately successful in enhancing the sensitivity of detection in techniques that depend on protonation to achieve ionisation such as electrospray ionisation (ESI) and MALDI analysis. These techniques are most effective if the analyte does not already possess a functionality with a high proton affinity, e.g. oligosaccharides (Okamoto et al., Anal Chem. 69(15): 2919-2926, "High-sensitivity detection and post-source decay of 2-aminopyridine-derivatized oligosaccharides with matrix-assisted laser desorption/ionisation mass spectrometry." 1997). However, analytes that already contain functionalities that are readily protonated, such as trypsin digested peptides, do not benefit significantly from such reagents and other methods to improve the sensitivity of these sorts of analyte are needed.

Various other reagents for derivatising peptides have also been developed. Reagents that introduce quaternary ammonium functionalities and quaternary phosphonium functionalities have been developed for positive ion mass spectrometry. Halogenated compounds, particularly halogenated aromatic compounds are well known electrophores, i.e. they pick up thermal electrons very easily. A variety of derivatisation reagents based on fluorinated aromatic compounds (Bian N. et al., Rapid Commun Mass Spectrom 11(16): 1781-1784, "Detection via laser desorption and mass spectrometry of multiplex electrophore-labelled albumin." 1997) have been developed for electron capture detection, which is a highly sensitive ionisation and detection process that can be used with negative ion mass spectrometry (Abdel-Baky S. & Giese R.W., Anal Chem 63(24):2986-2989, "Gas chromatography/electron capture negative-ion mass spectrometry at the zeptomole level." 1991). A fluorinated aromatic group could also be used as a sensitivity-enhancing group. Aromatic sulphonic acids have also been used for improving sensitivity in negative ion mass spectrometry.

Each type of derivatisation reagent that has been disclosed in the prior art has different benefits and limitations, which depend on the method of ionisation used and on the methods of mass analysis used (for a review see Roth et al., Mass Spectrometry Reviews 17:255-274, "Charge derivatisation of peptides for analysis by mass spectrometry", 1998). The mechanism by which sensitivity is enhanced may also be different for each type of group. Some derivatisation methods increase basicity and thus promote protonation and charge localisation, which improves sensitivity in surface desorption techniques like Matrix Assisted Laser Desorption Ionisation (MALDI) and Fast Atom Bombardment (FAB). So far, reagents that introduce charge-carrying functionalities or functionalities with high proton affinities have been developed for MALDI mass spectrometry but no reagents that improve the desorption of the analyte by increasing its ability to absorb light and to mix with the matrix have been reported.

Negative ion mass spectrometry is sometimes more sensitive because there is less background noise. A tag that can enhance both negative ion mode detection and positive ion mode detection would have significant advantages. A tag for uniformly improving sensitivity of all associated analytes has yet to be found for all mass spectrometry techniques and it is unlikely that a universal reagent will be found. However, for specific mass spectrometric techniques it should be possible to design reagents that take advantage of features of a particular technique to promote detection sensitivity.

In this invention, derivatisation reagents and methods for their use have been developed to enhance the sensitivity of detection by MALDI mass spectrometry and it is anticipated that the reagents should be effective for most analytes that may be detected by this technique. This technique even enhances detection of peptides that contain easily protonated functionalities such as amino and guanidino groups. The inventors have observed that coupling a MALDI matrix dye directly to a biomolecule such as a peptide prior to embedding that peptide in the free matrix will greatly enhance the sensitivity with which the peptide can be detected.

WO98/31830 describes arrays of cleavable labels that are detectable by mass spectrometry which identify the sequence of a covalently linked nucleic acid probe. These mass labels have a number of advantages over other methods of analysing nucleic acids. At present commercially favoured systems are based on fluorescent labelling of DNA. Fluorescent labelling schemes permit the labelling of a relatively small number of molecules simultaneously, typically 4 labels can be used simultaneously and possibly up to eight. However the costs of the detection apparatus and the difficulties of analysing the resultant signals limit the number of labels that can be used simultaneously in a fluorescence detection scheme. An advantage of using mass labels is the possibility of generating large numbers of labels which have discrete peaks in a mass spectrum allowing similar numbers of distinct molecular species to be labelled simultaneously. Fluorescent dyes are expensive to synthesize whereas mass labels can comprise relatively simple polymers permitting combinatorial synthesis of large numbers of labels at low cost. This application describes the use of mass-modified MALDI matrix molecules for the labelling of biomolecules. Tags comprising MALDI matrix agents such as cinnamic and sinapinic acid can be attached to biomolecules through a photocleavable linker allowing cleavage and desorption of tags within a laser desorption ionisation mass spectrometer without requiring additional matrix.

WO99/60007 discloses mass tags comprising trityl functionalities for the labelling of nucleic acids and oligonucleotides. These tags can be cleaved from their associated oligonucleotides by photolysis in a MALDI-TOF mass spectrometer prior to desorption. The cleavage product is charged which is advantageous as it improves the sensitivity of the detection of the tags. This method also does not require additional matrix.

The prior art therefore discloses methods and reagents for cleavable tags for use in MALDI mass spectrometry that may be desorbed without additional matrix. The present invention is distinguished by the fact that the tags are not cleaved from the analyte and that the tags are used in the presence of free matrix material. The absence of free matrix material is detrimental to the present invention.

It is an object of this invention to overcome the problems associated with the above prior art. In particular, it is an aim of this invention to provide methods and labels that can be used to produce improved peptide mass fingerprints and which will improve the sensitivity of detection of other labelled non-volatile macromolecules particularly other biomolecules such as nucleic acids.

It is a further object of this invention to provide compounds which have desirable features as mass labels, and methods for the use of those compounds to provide improved mass spectra of associated analytes.

Accordingly, the present invention provides a method for characterising an analyte by matrix assisted laser desorption ionisation (MALDI) mass spectrometry, which method comprises:

(a)   labelling the analyte with a light-absorbing label that absorbs light at a pre-determined frequency, to form a labelled analyte;

(b)   embedding the labelled analyte in a matrix formed from at least one compound that absorbs light, to form an embedded labelled analyte;

(c)   desorbing the embedded labelled analyte by exposing it to light having the pre-determined frequency, to form a desorbed analyte; and

(d)   detecting the desorbed analyte by mass spectrometry to characterise the analyte.

Thus, the presence of a light-absorbing label attached to the analyte causes the labelled analyte molecule to absorb energy, which in turn aids in energising the analyte to bring it into the gaseous phase where it can be detected by the mass spectrometer. Generally the substance or compound forming the matrix will also absorb the light and be brought into the gas phase at the same time as the analyte. Thus, it is advantageous in the present invention, if the light-absorbing label and/or the compound forming the matrix are rapidly desorbed on the application of light.

The advantage of the methods, (and the compounds and kits) of the present invention is that they contribute to improving sensitivity, and can increase the number of peptides (e.g. small peptides, which are not detectable in conventional MALDI experiments) that are detected from a protein. In addition, through the use of appropriate tags, it is possible with this invention to analyse multiple samples simultaneously and it is also possible to determine the ratios of corresponding peptides in the different samples. With appropriate labelling procedures, it is also possible facilitate the conditioning of polypeptide sample for detection by mass spectrometry.

In a preferred embodiment, the desorbed analyte is directly detected by mass spectrometry. In the context of the present invention, this means that it is the analyte itself that is detected by mass spectrometry, rather than some other moiety such as a mass label which is only relatable to the analyte. This embodiment is particularly preferred when one or more peptide mass fingerprints (PMFs) are being produced to characterise a protein, or a population o0f proteins.

Alternatively the desorbed analyte may be indirectly detected by mass spectrometry. In this embodiment the analyte is additionally labelled with a mass label relatable to the analyte. The mass label is preferably cleaved from the desorbed analyte before being fed into the mass spectrometer. The analyte is characterised by detecting the mass label and relating it to the analyte.

In the present invention, the light employed is not especially limited, provided that it is able to sufficiently excite the light-absorbing label and thus the analyte. Typically the light to which the embedded labelled analyte is exposed is a laser light. The frequency of the light is also not especially limited, and UV, visible or infrared light may be employed.

It is particularly preferred that the compound forming the matrix absorbs light at the same frequency as the light-absorbing label. This is efficient, since a single light source can be employed in the apparatus. One way of achieving this is to ensure that the matrix and the light-absorbing label are formed from the same compound. This is a preferred way of

practising the present invention. In this respect the final light-absorbing label and matrix-forming compound need not be identical (they cannot be, since one is attached chemically to the analyte) but should instead be substantially the same, or should comprise the same or similar groups such that they absorb light at the same, or substantially the same, wavelengths.

It is preferred that the light-absorbing label is formed from a dye, such as a non-fluorescent dye. The advantage of a non-fluorescent dye is that the energy absorbed is retained in the molecule to aid in the dissipation into the gas phase, rather than lost by re-emitance as fluorescence.

In the present invention, the analyte is not especially limited, and the invention may be employed to characterise any analyte. However, it is particularly well suited to biomolecules, such as proteins, polypeptides, peptides, peptide fragments and amino acids.

The methods of the present invention are useful in producing a PMF from a protein or polypeptide. Accordingly, the present invention also provides a method for characterising a polypeptide, which method comprises the steps of:

(a)   optionally reducing cysteine disulphide bridges in the polypeptide to form free thiols, and capping the free thiols;

(b)   cleaving the polypeptide with a sequence specific cleavage reagent to form peptide fragments;

(c)   optionally deactivating the cleavage reagent;

(d)   capping one or more ε-amino groups that are present with a lysine reactive agent;

(e)   analysing peptide fragments according to a method as defined above to form a mass fingerprint for the polypeptide; and

(f)   determining the identity of the polypeptide from the mass fingerprint.

When a population of proteins or polypeptides is to be investigated, the present invention can also be employed. In this respect, the present invention also provides a method for characterising a population of polypeptides, which method comprises the steps of:

(a)   optionally reducing cysteine disulphide bridges in one or more polypeptides to form free thiols, and capping the free thiols;

(b)   separating one or more polypeptides from the population;

(c)   cleaving one or more polypeptides with a sequence specific cleavage reagent to form peptide fragments;

(d)   optionally deactivating the cleavage reagent;

(e)   capping one or more ε-amino groups that are present with a lysine reactive agent;

(f)   analysing peptide fragments according to a method as defined above to form a mass fingerprint for one or more polypeptides; and

(g)   determining the identity of one or more polypeptides from the mass fingerprint.

The present invention can also be used to compare a number of protein or polypeptide samples. Thus, the present invention further provides a method for comparing a plurality of samples, each sample comprising one or more polypeptides, which method comprises the steps of:

(a)   optionally reducing cysteine disulphide bridges and capping the free thiols in one or more polypeptides from the samples;

(b)   separating one or more polypeptides from each of the samples;

(c)   cleaving the polypeptides with a sequence specific cleavage reagent to form peptide fragments;

(d)   optionally deactivating the cleavage reagent;

(e)   capping one or more ε-amino groups that are present with a lysine reactive agent;

(f)   analysing peptide fragments according to a method as defined above to form a mass fingerprint for one or more polypeptides from the samples; and

(g)   determining the identity of one or more polypeptides in the samples from one or more mass fingerprints.

In the latter three aspects of the present invention it is preferred that the lysine-reactive agent is a labelled lysine-reactive agent. The label can be employed to distinguish which proteins or polypeptides originate from which samples, so that the samples can be pooled for analysis where appropriate.

In these aspects of the present invention, the sequence specific cleavage agent cleaves the one or more polypeptides on the C-terminal side of a lysine residue. Preferably the specific cleavage reagent comprises Lys-C or Trypsin. It is also preferred that the peptide fragments having capped ε-amino groups are removed by affinity capture. This can be achieved by ensuring that the lysine reactive agent comprises biotin.

The most preferred lysine reactive agent for use in the present invention comprises a hindered Michael reagent. Typically the hindered Michael agent comprises a compound having the following structure:
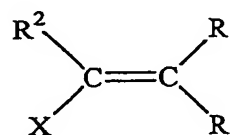
$$R^2\diagdown\text{C}=\text{C}\diagup R$$
$$X\diagup\qquad\diagdown R$$

wherein X is an electron withdrawing group that is capable of stabilising a negative charge; the R groups independently comprise a hydrogen, a halogen, an alkyl, an aryl, or an aromatic group with the proviso that at least one of the R groups comprises a sterically hindering group; and the group R^2 comprises a hydrogen, a halogen, a hydrocarbon group, an electron withdrawing group and/or a linker capable of attachment to an affinity capture functionality or a solid phase support.

The present invention also provides a compound for labelling an analyte, which compound has the following structure:
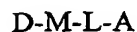
D-M-L-A

wherein D comprises a light absorbing label, M comprises a mass modifier, L comprises a linker and A comprises an analyte.

In a preferred embodiment of the present invention, D comprises a dye, such as a non-fluorescent dye. Typically, the non-fluorescent dye comprises a compound selected from 4-dimethylaminoazobenzine-4'-sulphonyl chloride (DABSYL chloride), 3-hydroxypicolinic acid, 2,5-dihydroxybenzoic acid and 4-hydroxy-alpha-cyanocinnamic acid. M may be any mass marker, and is not especially limited. Preferably M is selected from a compound formed from an aryl ether, and an oligomer formed from 2 or more aryl ether units.

The linker is not especially limited and preferably comprises a group selected from $-CR_2-CH_2-SO_2-$, $-N(CR_2-CH_2-SO_2-)_2$, $-NH-CR_2-CH_2-SO_2-$, $-CO-NH-$, $-CO-O-$, $-NH-CO-NH-$, $-NH-CS-NH-$, $-CH2-NH-$, $-SO2-NH-$, $-NH-CH2-CH2-$ and $-OP(=O)(O)O-$.

The analyte, A may be any analyte, as already discussed above in relation to the methods of the present invention. Preferably A is a biomolecule, such as a protein, a polypeptide, a peptide, a peptide fragment or an amino acid.

The present invention also provides a kit for characterising an analyte by matrix assisted laser desorption ionisation (MALDI) mass spectrometry, which kit comprises:

(a)   a light absorbing label having a reactive functionality for attaching the label to an analyte; and

(b)   a compound for forming a matrix, which compound absorbs light at the same frequency as the light-absorbing label.

The present invention will be described in further detail by way of example only with reference to the accompanying Figures, in which:

Figure 1 shows a schematic description of the synthesis of two MALDI matrix mass tags based on 4-hydroxy-alpha-cyano-cinnamic acid;

Figure 2 shows a High Performance Liquid Chromatography (HPLC) trace from the coupling reaction of a reactive tag of this invention with a synthetic peptide;

Figure 3 shows a MALDI TOF MS spectrum of the peptide mixture shown in Figure 1;

Figure 4 shows a MALDI TOF MS spectrum from the labelling reaction of a synthetic peptide with a reactive MALDI matrix mass tag that comprises a linker.

Figure 5a shows a schematic of the labelling protocol for beta-MSH;

Figure 5b shows the MALDI TOF mass spectrum of the unlabelled and undigested beta-MSH peptide;

Figure 6 shows spectra MALDI TOF for the unlabelled and labelled digests of beta-MSH;

Figure 7 shows MALDI TOF mass spectra of this peptide mixed in various molar ratios with the digest of unlabeled beta-MSH;

Figure 8 shows a number of MALDI TOF mass spectra for a serial dilution of a stock solution of 44 pmol of the labelled peptide comprising amino acids 7 to 11 of beta-MSH mixed with 180 pmols of digested and unlabeled beta-MSH - the first spectrum shows the MALDI TOF analysis of the stock solution;

Figure 9 shows a typical MALDI TOF peptide mass fingerprint mass spectrum for unlabelled BSA;

Figure 10 shows the results of a search for unmodified BSA peptides in the SWISSPROT database using the MS-Fit database search program;

Figure 11 shows a MALDI TOF peptide mass fingerprint mass spectrum for labelled BSA;

Figure 12 shows the results of a search for modified BSA peptides in the SWISSPROT database using the MS-Fit database search program;

Figure 13 shows a typical MALDI TOF peptide mass fingerprint mass spectrum for unlabelled GAPDH;

Figure 14 shows the results of a search for unmodified GAPDH peptides in the SWISSPROT database using the MS-Fit database search program;

Figure 15 shows a MALDI TOF peptide mass fingerprint mass spectrum for labelled GAPDH;

Figure 16 shows the results of a search for modified GAPDH peptides in the SWISSPROT database using the MS-Fit database search program;

Figure 17a shows the tag compound 6-[2-Cyano-3-(4-hydroxy-3-sulfonato-phenyl)-acryloylamino]-hexanoic acid-(2,5-dioxo-pyrrolidin-1-yl)-ester Sodium;

Figure 17b shows the tag compound N^{α}-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg$\omega\omega'$(Boc$_2$)-2,5-dioxo-pyrrolidine-1-yl ester;

Figure 17c shows the tag compound N^α-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg-$\omega\omega'$(Boc^2)-N-(6-amino-hexanoic acid-OSu-ester);

Figure 17d shows the tag compound 4-[2-Cyano-3-(4-hydroxy-phenyl)-acryloyl]-1-[5-(2,5-dioxo-pyrrolidine-1-yloxycarbonyl)-pentyl]-piperazine-1-ium hydrochloride;

Figure 18 shows a scheme for the synthesis of the tag compound 6-[2-Cyano-3-(4-hydroxy-3-sulfonato-phenyl)-acryloylamino]-hexanoic acid-(2,5-dioxo-pyrrolidin-1-yl)-ester Sodium shown in Figure 17a;

Figure 19 shows a scheme for the synthesis of the tag compound N^α-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg$^{\omega\omega'}$(Boc$_2$)-2,5-dioxo-pyrrolidine-1-yl ester shown in Figure 17b;

Figure 20 shows a scheme for the synthesis of the tag compound N^α-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg-$^{\omega\omega'}$(Boc$_2$)-N-(6-amino-hexanoic acid-OSu-ester) shown in Figure 17c; and

Figure 21 shows a scheme for the synthesis of the tag compound 4-[2-Cyano-3-(4-hydroxy-phenyl)-acryloyl]-1-[5-(2,5-dioxo-pyrrolidine-1-yloxycarbonyl)-pentyl]-piperazine-1-ium hydrochloride shown in Figure 17d.

The present invention will now be described in more detail.

In the present invention a label molecule of the following structure is employed for attaching the light-absorbing label (or dye) to the analyte of interest:

Dye –Reactive Functionality

where the dye is preferably non-fluorescent and preferably dissipates absorbed radiation thermally.

In a preferred embodiment the label molecules comprise the following structure:

Dye – Mass Modifier - Linker – Reactive Functionality

In either case, the reactive functionality is not especially limited, provided that it is suitable for attaching the label to the analyte of interest.

In a preferred aspect of this invention there is provided a method of analysing an analyte molecule comprising the steps of:

1. Labelling the analyte molecule with a dye that absorbs light of a predetermined frequency.
2. Embedding the labelled analyte molecule in a matrix comprising a dye that absorbs light at the frequency of the laser to be used in the desorption step.
3. Desorbing the labelled analyte by application of laser light of the predetermined frequency so as to effect sublimation of the matrix and thus also the labelled analyte.
4. Detecting ions formed during the desorption step by mass spectrometry.

In a further aspect of this invention these is provided a kit comprising:

1. A mass label molecule usable in the first aspect of this invention; and
2. A compatible MALDI matrix reagent.

MALDI matrix dyes

Various compounds have been found to be useful as matrices for MALDI analysis of large biomolecules. These compounds are generally characterised by a number of properties. The compounds generally have a strong extinction coefficient at the

frequency of the laser used for desorption. The compounds are also able to isolate analyte molecules in a solid solution and the compounds are sufficiently volatile to rapidly sublime when exposed to laser shots in the MALDI mass spectrometer. The subliming dye should vaporise rapidly in a jet that entrains the embedded analyte molecules and for most purposes this should take place without fragmentation of the analyte (although fragmentation may sometimes be desirable if structural information about the analyte is sought). However, a matrix should not be too volatile as experiments can sometimes take several hours and the analyte/matrix co-crystal must remain stable under vacuum in the ion source for this period of time. The property of volatility to laser irradiation can be measured approximately by determining the initial velocity of analyte ions generated by the matrix. It has been observed that higher initial velocities correspond to 'softer' ionisation, i.e. reduced fragmentation, (Karas M. & Glückmann M., J Mass Spectrom **34**: 467 – 477, "The initial ion velocity and its dependence on matrix, analyte and preparation method in Ultraviolet Matrix-assisted Laser Desorption/Ionisation", 1999) but high initial ion velocities of some matrices also correlates to rapid sublimation under vacuum.

Different matrices have different properties in terms of their ability to assist in the desorption of embedded analytes and in the subsequent sensitivity with which the analytes are detected. It has been found empirically that certain matrices are more appropriate for the analysis of particular analytes than others. For example, 3-hydroxypicolinic acid has been found to be most effective for analysing oligonucleotides (Wu et al., Rapid Commun. Mass Spectrom. **7**:142-146, "Matrix-assisted laser desorption time-of-flight mass spectrometry of oligonucleotides using 3-hydroxypicolinic acid as an ultra-violet sensitive matrix", 1993), while 2,5-dihydroxybenzoic acid and 4-hydroxy -alpha-cyano-cinnamic acid (HCCA) are both most effective for the analysis of peptides and proteins (Strupat et al., Int. J. Mass Spectrom. Ion Proc. **111**: 89 – 102, "2,5-dihydroxybenzoic acid: a new matrix for laser desorption/ionisation mass spectrometry", 1991; Beavis et al., Org. Mass Spectrom. **27**: 156–158, "α-cyano-4-hydroxy cinnamic acid as a matrix for matrix-assisted laser desorption mass spectrometry", 1992). Various cinnamic acid derivatives have been found to be effective for the analysis of proteins (Beavis R.C. & Chait B.T., Rapid

Commun Mass Spectrom 3(12): 432-435, "Cinnamic acid derivatives as matrices for ultraviolet laser desorption mass spectrometry of proteins." 1989) and the choice of matrix is dependant on the nature of the analyte, for example sinnapinic acid may be preferred over HCCA for large peptides and polypeptides, while HCCA is generally preferred for smaller peptides. 2,5-dihydroxybenzoic acid may produce less fragmentation than the cinnamic acid derivatives in some cases.

Most of the matrices discussed above have been acidic matrices. Basic matrices have also been developed and may be more appropriate for the analysis of acid-sensitive compounds (Fitzgerald et al., Anal Chem. 65(22): 3204-3211, "Basic matrices for the matrix-assisted laser desorption/ionisation mass spectrometry of proteins and oligonucleotides." 1993).

Infrared MALDI (IR-MALDI) is similar in principal to ultraviolet MALDI (UV-MALDI) in that analytes must be embedded in a matrix that preferably has a strong extinction coefficient at the frequency of the laser in the desorption instrument. Appropriate matrices tend to be different compounds from those used in UV-MALDI and liquid matrices are often used. Glycerol, urea, ice and succinic acid have all been shown to be effective matrices for IR-MALDI (Talrose et al., Rapid Commun Mass Spectrom 13(21): 2191-2198, "Insight into absorption of radiation/energy transfer in infrared matrix-assisted laser desorption/ionisation: the roles of matrices, water and metal substrates." 1999). However, some UV-MALDI matrices, such as cinnamic acid derivatives, also work as IR matrices (Niu et al., J Am. Soc. Mass Spectrom. 9:1 – 7, "Direct comparison of infrared and ultraviolet wavelength matrix-assisted laser desorption/ionisation mass spectrometry of proteins", 1998).

Liquid matrices for UV-MALDI have also been explored (Ring S. & Rudich Y., Rapid Commun Mass Spectrom 14(6): 515-519, "A comparative study of a liquid and a solid matrix in matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry and collision cross section measurements." 2000; Sze et al., J Am Soc Mass Spectrom 9(2): 166-174, "Formulation of matrix solutions for use in matrix-assisted laser

desorption/ionisation of biomolecules." 1998; Karas et al. Mass Spectrom Rev **10**: 335, 1991). The simplest examples of liquid matrices comprise solutions of the matrices used as solids. True liquid matrices are also known such as nitrobenzoyl alcohol. Both types of matrix have some advantages in terms of sample consistency, stability under vacuum and ease of handling, however solid matrices tend to be more sensitive. In the context of the present invention, the improvements in sensitivity may justify the use of liquid matrices. This may have particular advantages in the automation of sample preparation, as liquid handling robotics are widely available and the use of solutions of matrices, for solid matrix co-crystallisation, which readily clog dispensing devices can be avoided.

Reactive tags comprising dyes and MALDI matrix dyes

In the one aspect of this invention light-absorbing dye molecules attached to analytes are provided. Various dyes that are not conventionally used in MALDI mass spectrometry may be used with this invention. Some dyes that absorb strongly in UV frequencies are commercially available with reactive functionalites, e.g. 4-dimethylaminoazobenzene-4'-sulfonyl chloride (DABSYL Chloride, Sigma-Aldrich, Poole, Dorset, UK). This reagent and similar UV absorbing dyes that thermally dissipate luminal excitation are applicable with this invention.
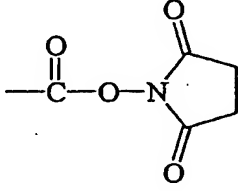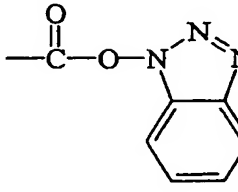
It is also possible to prepare reactive dyes from commercially available intermediates. A number of acidic matrices that are widely used for MALDI mass spectrometry, such as cinnamic, nicotinic and hydroxybenzoic acid derivatives, are commercially available. The acidic functionality in most of these reagents is a carboxylic acid group. This functionality may be readily converted to an active ester or acid chloride by conventional chemical methods (see for example Solomons, "Organic Chemistry", Fifth Edition published by Wiley). Preferred active esters include N-hydroxysuccinimide (NHS) esters and pentafluorophenyl esters. A variety of dyes will function in the methods of this invention, but preferred compounds absorb strongly in the frequency that is used for laser desorption in the mass spectrometer. Typically Ultra-Violet (UV) radiation is used. Infra-red lasers are also used for some MALDI applications.

Cinnamic acid derivatives are preferred dyes that are widely used in UV-MALDI TOF (Beavis RC, Chait BT, Rapid Commun Mass Spectrom 3(12):432-435, "Cinnamic acid derivatives as matrices for ultraviolet laser desorption mass spectrometry of proteins." 1989). A reactive derivative of cinnamic acid is discussed in the examples below. It is anticipated that this reagent may be applicable to both UV- and IR-MALDI.

Reactive Functionalities

A variety of other reactive functionalities may be appropriate to prepare reactive dyes for use with this invention. Table 1 below lists some reactive functionalities that may be incorporated into a dye molecule. These reactive functionalities may be reacted with nucleophilic functionalities which are found in biomolecules, particularly in peptides and· polypeptides. Reaction of the reactive functionalities with the nucleophilic functionalities shown generates a covalent linkage between the two entities. This covalent linkage is shown in the third column of the table. For applications involving synthetic oligonucleotides, primary amines or thiols are often introduced during the synthesis at the termini of the molecules to permit labelling. Any of the functionalities listed below could be introduced into the compounds of this invention to permit the mass markers to be attached to a molecule of interest. A reactive functionality can be used to introduce a further linker groups with a further reactive functionality if that is desired. Table 1 is not intended to be exhaustive and the present invention is not limited to the use of only the listed functionalities.

Table 1

Nucleophilic Functionality	Reactive Functionality	Resultant Linking Group
-SH	$-SO_2-CH=CR_2$	$-S-CR_2-CH_2-SO_2-$
$-NH_2$	$-SO_2-CH=CR_2$	$-N(CR_2-CH_2-SO_2-)_2$ or $-NH-CR_2-CH_2-SO_2-$
$-NH_2$ -OH		-CO-NH- -CO-O-
$-NH_2$ -OH		-CO-NH- -CO-O-
$-NH_2$	-NCO	-NH-CO-NH-
$-NH_2$	-NCS	-NH-CS-NH-
$-NH_2$	-CHO	$-CH_2-NH-$
$-NH_2$	$-SO_2Cl$	$-SO_2-NH-$
$-NH_2$	$CH_2=CH-$	$-NH-CH_2-CH_2-$
-OH	$-OP(NCH(CH_3)_2)_2$	$-OP(=O)(O)O-$

It should be noted that in applications involving labelling oligonucleotides with the mass markers of this invention, some of the reactive functionalities above or their resultant linking groups might have to be protected prior to introduction into an oligonucleotide synthesiser. Preferably unprotected ester, thioether and thioesters, amine and amide bonds are to be avoided, as these are not usually stable in an oligonucleotide synthesiser. A wide variety of protective groups is known in the art which can be used to protect linkages from unwanted side reactions. Alternatively, amine functionalised oligonucleotides can be prepared using standard methods known in the art and these can be labelled with amine reactive reagents such as NHS-esters.

Analysis of labelled biomolecules

In the second aspect of this invention, a method of detecting biomolecules is provided. In this method the biomolecules are covalently labelled with a dye molecule. The labelled molecules are then embedded in a MALDI matrix of a further dye molecule, which may be the same or different from the dye used to label the biomolecule. The labelled and embedded biomolecules are then analysed in a MALDI mass spectrometer. The dye used to label the analyte biomolecule and the dye chosen as a free matrix are both chosen to absorb light strongly in the frequency used for the MALDI process. Typically, laser Ultra-Violet (UV) frequencies of 266 nm (Nd-YAG lasers) or 337 nm (Nitrogen Lasers) are used.

Peptides and proteins are preferred biomolecules that benefit from the methods of this invention. A polypeptide or peptide or mixtures of polypeptides or peptides can be isolated for analysis by any of the conventional means such as electrophoresis, chromatography or affinity chromatography. For the purposes of mass spectrometry, it is preferred that polypeptides or proteins are not contaminated with salts or detergents, particularly metal salts. Various techniques for desalting a polypeptide or peptide mixture are known in the art such as gel filtration, dialysis or the use of hydrophobic resins. A particularly convenient and simple method for de-salting peptides involves aspiration of a small quantity of a solution of the peptide or polypeptide mixture in a pipette tip incorporating C18 packing materials. Salts and detergents will be removed first, substantially improving the detection sensitivity of the analysis of the peptides. Pipette tips pre-packaged with appropriate resins and instructions for their use are commercially available from Millipore (Bedford, MA, USA) under the trademark 'Zip Tip'. Desalting procedures may take place after labelling of the analyte to remove unreacted tags, if preferred.

Proteins contain various nucleophilic functionalities that can be labelled using reagents that are reactive to these functionalities. Proteins typically contain thiol, amino, hydroxyl and imidazole groups. These may all be labelled with appropriate reagents if desired. In preferred embodiments of this invention, amino groups are labelled. Amino groups may

be labelled with a variety of labels but acid chlorides and active esters are usually the most selective reactive functionalities. Preferred UV-absorbing dyes for use with this invention include active esters of cinnamic acid and its derivatives, active esters of nicotinic acid or active esters of hydroxybenzoic acid derivatives. Thus, in one embodiment of the second aspect of this inventions, isolated peptides in a mixture are labelled with an active ester of 4-hydroxy-alpha-cyano-cinnamic acid. The peptides are desalted using a Zip tip and then embedded in a matrix of unmodified 4-hydroxy-alpha-cyano-cinnamic acid. Typically, a solution of the matrix is prepared in a volatile solvent such as acetonitrile containing a small amount of trifluoroacetic acid (0.1 to 0.5% by volume is sufficient). This solution is then pipetted onto a metal target to form small droplets. A small quantity of the desalted, labelled peptide solution is then dropped into the droplet of matrix solution. This solution is then left to dry so that the peptides can co-crystallise with the matrix. In other techniques the matrix solution is allowed to dry and crystallise before the peptide solution is added on top (Hutchens and Yip, Rapid Commun. Mass Spectrom. 7: 576 – 580, 1993). This procedure may also be repeated to produce layers of co-crystallised analyte and matrix. These and other variations of the co-crystallisation technique may be used to improve the analysis of peptides or polypeptides. Liquid matrices, as discussed above may also be used. The matrix/peptide co-crystals are then analysed by laser desorption in a MALDI-TOF mass spectrometer.

Mass Spectrometers

The essential features of a mass spectrometer are as follows

Inlet System -> Ion Source -> Mass Analyser -> Ion Detector -> Data Capture System

There are various inlet systems, ion sources and mass analysers that can be used for the purposes of analysing large biomolecules but in the context of this invention the ion source is a Matrix Assisted Laser Desorption ion source for which there are only a limited number of inlet systems. A variety of mass analysers, ion detectors and data capture systems may be used with MALDI although some mass spectrometer geometries are not commercially produced. Time-of-flight mass analysers are typically used with MALDI as

well as Fourier Transform Ion Cyclotron Resonance mass analysers and Quadrupole/Time-of-flight mass analysers. In principle ion traps and sector instruments can be used with MALDI but generally these are not commercially produced.

Inlet Systems

Moving belt systems are one of the few inlet systems that have been used with laser desorption for the analysis of labelled nucleic acids (Linxiao Xu et al., Anal. Chem. 69: 3595 – 3602, "Electrophore Mass Tag Dideoxy DNA sequencing", 1997). Although this technology has not been used with MALDI it should be trivial to adapt such interfaces for use with the reagents and methods of this invention.

Matrix Assisted Laser Desorption Ionisation (MALDI)

MALDI requires that the biomolecule solution be embedded in a large molar excess of a photo-excitable 'matrix'. The application of laser light of the appropriate frequency results in the excitation of the matrix which in turn leads to rapid evaporation of the matrix along with its entrapped biomolecule. Proton transfer from the acidic matrix to the biomolecule gives rise to protonated forms of the biomolecule which can be detected by positive ion mass spectrometry, particularly by Time-Of-Flight (TOF) mass spectrometry. Negative ion mass spectrometry is also possible by MALDI TOF. This technique imparts a significant quantity of translational energy to ions, but tends not to induce excessive fragmentation despite this. The laser energy and the timing of the application of the potential difference used to accelerate the ions from the source can be used to control fragmentation with this technique. This technique is highly favoured for the determination of peptide mass fingerprints due to its large mass range, due to the prevalence of singly charged ions in its spectra and due to the ability to analyse multiple peptides simultaneously.

The photo-excitable matrix comprises a 'dye' , i.e. a compound that strongly absorbs light of a particular frequency, and which preferably does not radiate that energy by fluorescence or phosphorescence but rather dissipates the energy thermally, i.e. through vibrational modes. It is the vibration of the matrix caused by laser excitation that results

in rapid sublimation of the dye which simultaneously takes the embedded analyte into the gas phase.

Mass Analysers

Time-of-Flight Mass Analysers

As the name implies, Time-of-flight mass analysers measure the time it takes for ions to travel a predetermined distance under the influence of a predetermined potential difference. The time-of-flight measurement allows the mass-to-charge ratio of ions striking a detector to be calculated. These instruments measure the arrival of almost all of the ions in a sample and as a result can be quite sensitive although, selectivity with this technique is more difficult to achieve. This technique can also detect ions with higher mass-to-charge ratios than can typically be measured in an ion trap or quadrupole mass spectrometer. TOF mass analysers are presently widely used with MALDI.

Ion Traps

Ion Trap mass analysers are related to the quadrupole mass analysers. The ion trap generally has a 3-electrode construction - a cylindrical electrode with 'cap' electrodes at each end forming a cavity. A sinusoidal radio frequency potential is applied to the cylindrical electrode while the cap electrodes are biased with DC or AC potentials. Ions injected into the cavity are constrained to a stable circular trajectory by the oscillating electric field of the cylindrical electrode. However, for a given amplitude of the oscillating potential, certain ions will have an unstable trajectory and will be ejected from the trap. A sample of ions injected into the trap can be sequentially ejected from the trap according to their mass/charge ratio by altering the oscillating radio frequency potential. The ejected ions can then be detected allowing a mass spectrum to be produced.

Ion traps are generally operated with a small quantity of a 'bath gas', such as helium, present in the ion trap cavity. This increases both the resolution and the sensitivity of the device as the ions entering the trap are essentially cooled to the ambient temperature of the bath gas through collision with the bath gas. Collisions both increase ionisation when

a sample is introduced into the trap and dampen the amplitude and velocity of ion trajectories keeping them nearer the centre of the trap. This means that when the oscillating potential is changed, ions whose trajectories become unstable gain energy more rapidly, relative to the damped circulating ions and exit the trap in a tighter bunch giving a narrower larger peaks.

Ion traps can mimic tandem mass spectrometer geometries, in fact they can mimic multiple mass spectrometer geometries allowing complex analyses of trapped ions. A single mass species from a sample can be retained in a trap, i.e. all other species can be ejected and then the retained species can be carefully excited by super-imposing a second oscillating frequency on the first. The excited ions will then collide with the bath gas and will fragment if sufficiently excited. The fragments can then be analysed further. It is possible to retain a fragment ion for further analysis by ejecting other ions and then exciting the fragment ion to fragment. This process can be repeated for as long as sufficient sample exists to permit further analysis. It should be noted that these instruments generally retain a high proportion of fragment ions after induced fragmentation. These instruments and FTICR mass spectrometers (discussed below) represent a form of temporally resolved tandem mass spectrometry rather than spatially resolved tandem mass spectrometry which is found in linear mass spectrometers.

Fourier Transform Ion Cyclotron Resonance Mass Spectrometry (FTICR MS)

FTICR mass spectrometry has similar features to ion traps in that a sample of ions is retained within a cavity but in FTICR MS the ions are trapped in a high vacuum chamber by crossed electric and magnetic fields. A pair of plate electrodes that form two sides of a box generates the electric field. The box is contained in the field of a superconducting magnet which in conjunction with the two plates, the trapping plates, constrain injected ions to a circular trajectory between the trapping plates, perpendicular to the applied magnetic field. The ions are excited to larger orbits by applying a radio-frequency pulse to two 'transmitter plates', which form two further opposing sides of the box. The cycloidal motion of the ions generates corresponding electric fields in the remaining two opposing sides of the box, which comprise the 'receiver plates'. The excitation pulses

excite ions to larger orbits which decay as the coherent motions of the ions is lost through collisions. The corresponding signals detected by the receiver plates are converted to a mass spectrum by Fourier Transform (FT) analysis.
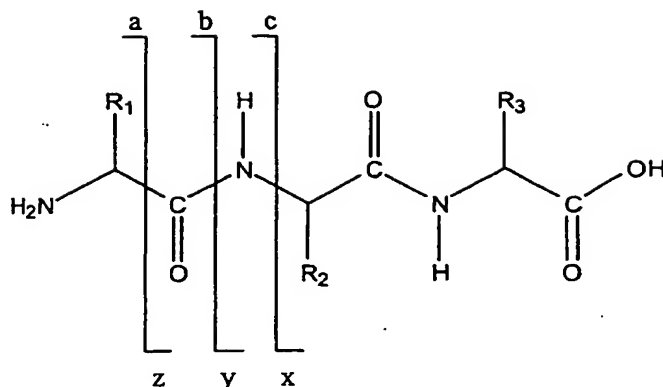
For induced fragmentation experiments these instruments can perform in a similar manner to an ion trap - all ions except a single species of interest can be ejected from the trap. A collision gas can be introduced into the trap and fragmentation can be induced. The fragment ions can be subsequently analysed.

Analysis of peptides by mass spectrometry

Fragmentation of peptides by collision induced dissociation, to determine their sequence, may be used in this invention to identify proteins, not identified by the pattern of masses of their digestion products. In addition, fragmentation can also be obtained by photo-excitation or by electron impact. Various mass analyser geometries may be used to fragment peptides and to determine the mass of the fragments.

MS/MS and MS^n analysis of peptides

Tandem mass spectrometers allow ions with a pre-determined mass-to-charge ratio to be selected and fragmented (by collision induced dissociation (CID), for example). The fragments can then be detected providing structural information about the selected ion. When peptides are analysed by CID in a tandem mass spectrometer, characteristic cleavage patterns are observed, which allow the sequence of the peptide to be determined. Natural peptides typically fragment randomly at the amide bonds of the peptide backbone to give series of ions that are characteristic of the peptide. CID fragment series are denoted a_n, b_n, c_n, etc. for cleavage at the nth peptide bond where the charge of the ion is retained on the N-terminal fragment of the ion. Similarly, fragment series are denoted x_n, y_n, z_n, etc. where the charge is retained on the C-terminal fragment of the ion.

```
         a      b     c
         R₁     H     O     R₃
                      ‖
H₂N      C      N     C      N      C   OH
         ‖            |      |      ‖
         O     R₂     H      H      O
         z      y     x
```

Trypsin, Lys-C and thrombin are favoured cleavage agents for tandem mass spectrometry as they produce peptides with basic groups at both ends of the molecule, i.e. the alpha-amino group at the N-terminus and lysine or arginine side-chains at the C-terminus. This favours the formation of doubly charged ions, in which the charged centres are at opposite termini of the molecule. These doubly charged ions produce both C-terminal and N-terminal ion series after CID. This assists in determining the sequence of the peptide. Generally speaking only one or two of the possible ion series are observed in the CID spectra of a given peptide. In low-energy collisions typical of quadrupole based instruments the b-series of N-terminal fragments or the y-series of C-terminal fragments predominate. If doubly charged ions are analysed then both series are often detected. In general, the y-series ions predominate over the b-series.

In general peptides fragment via a mechanism that involves protonation of the amide backbone follow by intramolecular nucleophilic attack leading to the formation of a 5-membered oxazolone structure and cleavage of the amide linkage that was protonated (Schlosser A. and Lehmann W.D. J. Mass Spectrom. 35: 1382-1390, "Five-membered ring formation in unimolecular reactions of peptides: a key structural element controlling low-energy collision induced dissociation", 2000). Figure 16a shows one proposed mechanism by which this sort of fragmentation takes place. This mechanism requires a carbonyl group from an amide bond adjacent to a protonated amide on the N-terminal side of the protonated amide to carry out the nucleophilic attack. A charged oxazolonium ion gives rise to b-series ions, while proton transfer from the N-terminal fragment to the

C-terminal fragment gives rise to y-series ions as shown in Figure 16a. This requirement for an appropriately located carbonyl group does not account for cleavage at amide bonds adjacent to the N-terminal amino acid, when the N-terminus is not protected and, in general, b-series ions are not seen for the amide between the N-terminal and second amino acid in a peptide. However, peptides with acetylated N-termini do meet the structural requirements of this mechanism and fragmentation can take place at the amide bond immediately after the first amino acid by this mechanism. Peptides labelled on lysine or at an alpha-amino group with active ester tags of this invention should not undergo significant cleavage at the tag peptide during low energy CID analysis if there is no appropriately located carbonyl group in the tag molecule. This means that CID spectra for labelled peptides should be similar to the spectra for unlabelled peptides although the spectra will show mass shifts corresponding to multiples of the mass of the tag. This can be readily compensated for in the analysis of such CID spectra.

A typical tandem mass spectrometer geometry is a triple quadrupole which comprises two quadrupole mass analysers separated by a collision chamber, also a quadrupole. This collision quadrupole acts as an ion guide between the two mass analyser quadrupoles. A gas can be introduced into the collision quadrupole to allow collision with the ion stream from the first mass analyser. The first mass analyser selects ions on the basis of their mass/charge ration which pass through the collision cell where they fragment. The fragment ions are separated and detected in the third quadrupole. Induced cleavage can be performed in geometries other than tandem analysers. Ion trap mass spectrometers can promote fragmentation through excitation of a defined m/z range resulting in collision with the bath gas. Ion traps generally contain a bath gas, such as helium. Similarly photon induced fragmentation could be applied to trapped ions. Another favourable geometry is a Quadrupole/Orthogonal Time of Flight tandem instrument where the high selectivity of the quadrupole is coupled to the high sensitivity of a reflectron TOF mass analyser to identify the products of fragmentation.

Conventional 'sector' instruments are another common geometry used in tandem mass spectrometry. A sector mass analyser comprises two separate 'sectors', an electric sector

which focuses an ion beam leaving a source into a stream of ions with the same kinetic energy using electric fields. The magnetic sector separates the ions on the basis of their mass to generate a spectrum at a detector. For tandem mass spectrometry a two sector mass analyser of this kind can be used where the electric sector provide the first mass analyser stage, the magnetic sector provides the second mass analyser, with a collision cell placed between the two sectors. Two complete sector mass analysers separated by a collision cell can also be used for analysis of mass tagged peptides.

Affinity Capture Ligands

In certain embodiments of this invention the mass markers comprise an affinity capture ligand. Affinity capture ligands are ligands, which have highly specific binding partners. These binding partners allow molecules tagged with the ligand to be selectively captured by the binding partner. Preferably a solid support is derivitised with the binding partner so that affinity ligand tagged molecules can be selectively captured onto the solid phase support. The use of an affinity capture ligand provides many advantages, in that tagged species can be selectively captured prior to analysis allowing separation of tagged and untagged material while also allowing for conditioning of the analyte for mass spectrometry. Conditioning of a sample may include removal of detergents and other contaminants that can suppress ionisation or otherwise interfere with mass spectrometry. Conditioning also includes removal of salts that may form adducts with analytes causing mass shifts in the mass spectrum. In addition, pH may be adjusted to optimise ionisation. Conditioning of tagged analytes captured onto a solid phase support is trivial as the captured material can be easily washed with an appropriate buffer comprising volatile salts such as ammonium carbonate or trifluoroacetic acid depending on the desired pH. This washing step can remove contaminants and can be used to adjust the pH appropriately.

A further advantage of the inclusion of an affinity ligand is the ability to selectively isolate certain analyte species if the tag additionally comprises a reactive functionality that will couple the affinity ligand to specific analytes. For example, Gygi et al. (Nature Biotechnology 17: 994 – 999, 1999) disclose the use of 'isotope encoded affinity tags'

(ICAT) for the capture of peptides from proteins, to allow protein expression analysis. The authors report that a large proportion of proteins (>90%) in yeast have at least one cysteine residue (on average there are ~5 cysteine residues per protein). Reduction of disulphide bonds in a protein sample and capping of free thiols with iodoacetamidylbiotin results in the labelling of all cysteine residues. The labelled proteins are then digested, with trypsin for example, and the cysteine-labelled peptides may be isolated using avidinated beads. These captured peptides can then be analysed by liquid chromatography tandem mass spectrometry (LC-MS/MS) to determine an expression profile for the protein sample. Two protein samples can be compared by labelling the cysteine residues with a different isotopically modified biotin tag. In a useful embodiment of this invention, isotopically differentiated, cysteine reactive tags of this invention comprising an affinity ligand may be employed to improve the sensitivity of the ICAT analysis method. Similarly, Schmidt and Thompson (WO 98/32876) disclose the use biotin reagents to capture C- or N-terminal peptides for protein expression profiling analysis by mass spectrometry. The sensitivity of this process would also be enhanced by tags of this invention comprising an affinity ligand.

A preferred affinity capture ligand is biotin, which can be introduced into the tags of this invention by standard methods known in the art. In particular a lysine residue may be incorporated after amino acid 2 through which an amine-reactive biotin can be linked to the peptide mass tags (see for example Geahlen R.L. et al., Anal Biochem 202(1): 68-67, "A general method for preparation of peptides biotinylated at the carboxy terminus." 1992; Sawutz D.G. et al., Peptides 12(5): 1019-1012, "Synthesis and molecular characterization of a biotinylated analog of [Lys]bradykinin." 1991; Natarajan S. et al., Int J Pept Protein Res 40(6): 567-567, "Site-specific biotinylation. A novel approach and its application to endothelin-1 analogs and PTH-analog.", 1992). Iminobiotin and desthiobiotin are also applicable. A variety of avidin counter-ligands for biotin are available, which include monomeric and tetrameric avidin and streptavidin, all of which are available on a number of solid supports.

Other affinity capture ligands include digoxigenin, fluorescein, nitrophenyl moieties and a number of peptide epitopes, such as the c-myc epitope, for which selective monoclonal antibodies exist as counter-ligands. Metal ion binding ligands such as hexahistidine, which readily binds Ni^{2+} ions, are also applicable. Chromatographic resins, which present iminodiacetic acid chelated Ni^{2+} ions are commercially available, for example. These immobilised nickel columns may be used to capture tagged peptide, which comprise oligomeric histidine. As a further alternative, an affinity capture functionality may be selectively reactive with an appropriately derivitised solid phase support. Boronic acid, for example, is known to selectively react with vicinal cis-diols and chemically similar ligands, such as salicylhydroxamic acid. Reagents comprising boronic acid have been developed for protein capture onto solid supports derivitised with salicylhydroxamic acid (Stolowitz M.L.. et al., Bioconjug Chem **12**(2): 229-239, "Phenylboronic Acid-Salicylhydroxamic Acid Bioconjugates. 1. A Novel Boronic Acid Complex for Protein Immobilization." 2001; Wiley J.P. et al., Bioconjug Chem **12**(2): 240-250, "Phenylboronic Acid-Salicylhydroxamic Acid Bioconjugates. 2. Polyvalent Immobilization of Protein Ligands for Affinity Chromatography." 2001, Prolinx, Inc, Washington State, USA). It is anticipated that it should be relatively simple to link a phenylboronic acid functionality to the tags of this invention to generate capture reagents that can be captured by selective chemical reactions. The use of this sort of chemistry would not be directly compatible with biomolecules bearing vicinal cis-diol-containing sugars, however these sorts of sugars could be blocked with phenylboronic acid or related reagents prior to reaction with boronic acid derivitised tag reagents.

Charge derivatisation of peptides

In some embodiments of the this invention the tags may comprise readily ionisable groups, which can assist both in solubilisation of the tag and tagged analytes and in ionisation of the tagged analytes in the mass spectrometer. Various functionalities can be used as ionisable groups. The tertiary amino group and the guanidino group are both useful functionalities for solubilisation and ionisation (Francesco L. Branca, Stephen G. Oliver and Simon J. Gaskell, Rapid Commun. in Mass Spec., **14**, 2070-2073, "Improved

matrix-assisted laser desorption/ionisation mass spectrometric analysis of tryptic hydrolysates of proteins following guanidination of lysine-containing peptides." 2000).

Various other methods for derivatising peptides have been also been developed. These include the use of quaternary ammonium derivatives, quaternary phosphonium derivatives and pyridyl derivatives for positive ion mass spectrometry. Each type of ionisable functionality has different benefits, which depend on the method of ionisation used and on the methods of mass analysis used. Some derivitisation reagents increase basicity and thus promote protonation and/or charge localization for positive ion mass spectrometry while other reagents readily lose protons making them appropriate for negative ion mass spectrometry, which is often more sensitive than positive ion mass spectrometry because there is less background noise. Charge derivitisation can also change the fragmentation products of derivatised peptides, when collision induced dissociation is used. In particular some derivatisation techniques simplify fragmentation patterns, which is highly advantageous, if peptides are to be analysed by techniques such as collision induced dissociation. The choice of ionising functionality will be determined by the mass spectrometric techniques that will be employed (for a review see Roth et al., Mass Spectrometry Reviews 17:255-274, "Charge derivatisation of peptides for analysis by mass spectrometry", 1998). For the purposes of this invention ionising functions that promote positive or negative ion formation are equally applicable.

Charged groups such as tertiary amino functionalities, guanidino functionalities and sulphonic acid functionalities provide an additional advantage. These groups can act as affinity ligands allowing tagged analytes to be purified by ion exchange. Tags comprising guanidino and tertiary amino functions can be captured onto a strong cation exchange resin allowing conditioning prior to mass spectrometry analysis. Similarly, tags comprising sulphonic acid functions can be captured onto anion exchange resins allowing conditioning prior to mass spectrometry analysis. Additionally, the interaction between unreacted tags and the resin, anion or cation exchange, is weaker than the interaction of tagged analytes allowing unreacted tag to be readily washed away. The tagged analytes can be eluted with an appropriate buffer comprising a suitable concentration of a volatile

acid, base or salt depending on the resin. Accordingly, it is envisaged that pipette tips, spin columns and cartridges packed with a cation exchange resin or an anion exchange resin will be useful tools for the preparation of labelled samples to allow facile clean-up of the labelled peptides prior to analysis.

In addition sulphonic acid groups are advantageous for MALDI TOF analysis. Sulphonic acid derivatives of the alpha-amino functionality of peptides have been shown to enhance fragmentation efficiency in MALDI-Ion Trap analysis of peptides with improved spectra for certain classes of peptides that typically give poor MS/MS spectra in the ion trap, such as peptides containing aspartic and glutamic acid (Keough, T., Lacey M. P., et al., Rapid Commun Mass Spectrom 15(23): 2227-2239, "Atmospheric pressure matrix-assisted laser desorption/ionisation ion trap mass spectrometry of sulphonic acid derivatised tryptic peptides.", 2001). The strongly acidic functionality facilitates protonation of the amide backbone of singly charged peptides in MALDI leading to increased fragmentation.

In specific embodiments of this invention, tags comprising guanidino groups and sulphonic acid groups have been synthesized, see figures 17, 18 and 19 and the examples section. In general preferred charged groups include guanidino groups, tertiary amino groups and sulphonic acid groups.

Surface Enhanced Laser Desorption Ionisation

Surface Enhanced Laser Desorption Ionisation (SELDI) is a variant of MALDI in which the usual metal targets for MALDI are derivatised (Weinberger S.R., Morris T.S., Pawlak M., Pharmacogenomics 1(4):395-416 "Recent trends in protein biochip technology.", 2000). These surface modifications include derivatisation with anion exchangers, cation exchangers, hydrophobic surfaces or hydrophilic surfaces. When protein or peptide samples are applied to these surfaces, the sample adsorbs to the surface and with appropriate washing steps, fractions of the sample can be selectively removing leaving specific components on the target for further analysis by MALDI TOF mass spectrometry. It is envisaged that this may be a useful technique to apply with the labels

of this invention, both for analytical purposes and for separating labelled analytes from unreacted tags, particularly surfaces coated with cation or anion exchange resins.

The present invention will be described in further detail by way of example only with reference to the following specific embodiments.

Examples

Example 1 - Synthesis of amine-reactive derivatives of 4-hydroxy-alpha-cyano-cinnamic acid

Two different reactive derivatives of 4-hydroxy-alpha-cyano-cinnamic acid (HCCA) were synthesised. The first derivative prepared was the N-hydroxysuccinimide (NHS) ester of the carboxyl function of HCCA. The NHS ester of HCCA (NHS-HCCA) is an amine reactive derivative (see Figure 1). The first synthesis was successful and gave good results on the MALDI but the yield of the reaction with peptides was not as good as desired so a second synthesis was devised to provide a derivative of HCCA which incorporated a spacer between the cinnamic acid functionality and the reactive NHS ester group. This second reagent (see Figure 1) will be referred to as NHS-L-HCCA is also amine reactive.

Example 2 - Synthesis of 2-cyano-3-(4-tert-butoxycarbonyloxyphenyl) acrylic acid N-hydroxysuccinimide ester [NHS-HCCA]

The synthesis of NHS-HCCA is shown in Figure 1. In the first step the hydroxyl function of HCCA is protected followed by activation of the carboxylic acid moiety.

Example 2a - Synthesis of 2-cyano-3-(4-tert-butoxycarbonyloxyphenyl) acrylic acid

5.6g (30 mmol) of 2-cyano-3-(4-hydroxyphenyl) acrylic acid dissolved in 40 ml acetonitrile were stirred with 4.6 ml (33 mmol) of triethylamine until a clear solution was obtained. 0.2 g (4 mmol) 4-dimethylaminopyridine and 7.3 g (33 mmol) *tert*-butylpyrocarbonate were then added to the clear solution. After 2 hours reaction (the

solution is at that point colourless), the solution was reduced to its half volume and washed with 200 ml of a cold 5% citric acid solution.

The organic layer was extracted by ethyl acetate. After evaporation of the solvent, the product was precipitated from heptane/ethyl acetate.

Yield: 7.4 = 85%

Melting Point: 120–121°C

Example 2b - Synthesis of 2-cyano-3-(4-tert-butoxycarbonyloxyphenyl) acrylic acid N-hydroxysuccinimide ester

0.95 g (5 mmol) 2-cyan-3-(4-tert-butoxycarbonyloxyphenyl) acrylic acid and 0.6 g (5 mmol) N-hydroxysuccinimide were dissolved in 10 ml acetonitrile. 1.1 g (5.7 mmol) N-ethyl-N'-3-dimethylaminodicyclohexylcarbodiimide hydrochloride were added in portions to the reaction mixture. After 2 hours, the solvent was evaporated. The residue obtained was washed with ethyl acetate and with a cold 5 % citric acid solution and then with a saturated NaCl solution. The product was purified by chromatography.

Yield: 1.2g=63%

Example 3 - Synthesis of 2-cyano-3-(4-hydroxyphenyl) acrylic acid (6-[2,5-dioxo-pyrrolidinyl-N-oxy]-6-oxo) hexyl amide [NHS-L-HCCA]

The synthesis of NHS-L-HCCA is shown in Figure 1. In the first step a chlorinated linker is produced. The chlorine group is then nucleophilically substituted by a cyanide ion. This cyano linker is then condensed with 4-hydroxybenzaldehyde to give a cinnamic acid derivative with a six carbon chain linker with a free carboxyl group that is activated to form an NHS-ester in the final step of the synthesis.

Example 3a - Synthesis of 6-(chloracetamido) hexanoic acid

18 ml (221 mMol) chloracetylchloride was added dropwise to 20 g (153 mmol) 6-aminohexanoic acid dissolved in 80 ml cold NaOH solution (2N) at room temperature

(RT). The reaction mixture was stirred for 30 minutes while the pH of the solution was kept between 10-11 with occasional addition of NaOH solution (6N). The pH of the reaction mixture was then altered to pH 5 with HCl (2N) and the residue was filtered. The residue was then washed with water until the pH of the water was neutral. The product, dried over phosphorus pentoxide, was re-dissolved in 300 ml chloroform and filtered to remove the undissolved residue. Heptane was added to the filtrate and a syrup was obtained by stirring under cooling. The product was filtered, dried and was then crystallized from water.

Yield: 20 g=63 %
Melting Point: 82°C

Example 3b - Synthesis of 6-(cyanoacetamido) hexanoic acid

2.8 g (20 mmol) potassium hydrogen carbonate were added to 8.3 g (40 mmol) 6-(chloracetamido) hexanoic acid dissolved in 25 ml water. 3.2 g (48 mmol) potassium cyanide was then added to the clear solution which was cooled on ice. The reaction mixture was stirred for 17 hours and was then acidified with HCl (2N). The residue after extraction was purified by chromatography (silica gel, solvent: ethyl acetate).

Yield: 6g=76 %
Melting Point: 80-81°C

Example 3c - Synthesis of 2-cyano-3-(4-hydroxyphenyl) acrylic acid (6-hydroxy-6-oxo-hexyl)amide

7.5 g (38 mmol 6-(cyanacetamido) hexanoic acid was dissolved in 50 ml pyridine. 4.6 g (38 mmol) 4-hydroxybenzaldehyde and 0.7 ml (7 mmol) piperidine were added to the solution and the reaction mixture was stirred for 2 hours at 50°C. A further aliquot of 0.4 ml piperidine was then added to the reaction and the solution was stirred at RT for 60 hours. The residue after evaporation of the pyridine was acidified with HCl (2N) and was extracted with ethyl acetate. The organic layer was poured into 300 ml of a saturated solution of sodium hydrogen carbonate. The aqueous layer was then carefully acidified

with HCl (2N). The precipitated residue was filtered and washed with water. The dried product was crystallized from dioxane.

Yield: 8.4g=74 %

Melting Point: 178°C

Example 3d - Synthesis of 2-cyano-3-(4-hydroxyphenyl) acrylic acid (6-[2,5-dioxo-pyrrolidinyl-N-oxy]-6-oxo) hexyl amide

2.3g (20mmol) N-hydroxysuccimide and 6.0g (20 mmol) 2-Cyan-3-(4-hydroxyphenyl) acrylic acid [6-hydroxy –6-oxo-hexyl] amide were dissolved in 200°ml dioxane at 60-70°C. 4.6g (22 mmol) of dicyclohexylcarbodiimide was added to the reaction mixture which was stirred and cooled to 30°C. This temperature was maintained for one hour. The reaction mixture was then brought to room temperature and stirred for 20 hours. The solution was filtered and evaporated. The residue was treated with dichloromethane and a solution of sodium bicarbonate. The organic layer after extraction was washed with water and dried over sodium sulphate. After evaporation of the solvent, the residue was then chromatographed on silica gel. The product was crystallised from ethyl acetate. To avoid the exothermic reaction caused by depositing the product onto silica gel, the column was first cooled.

Yield: 50g=63%

Melting Point: 142°C

*Example 4 - Reaction of NHS-HCCA with Resin-bound Peptide*

The first active ester cinnamic acid mass tag (NHS-HCCA), whose synthesis is described above, was attached to resin bound peptides according to the following procedure.

Target Peptide

The peptide sequence, HRDPYRFDPHKD, was synthesised on a Wang type resin using standard Fmoc/tBu synthesis procedures (see for example Fields G.B. & Noble R.L., Int J Pept Protein Res 35(3): 161-214, "Solid phase peptide synthesis utilizing

9-fluorenylmethoxycarbonyl amino acids." 1990). The resin-bound peptide yields a free acid moiety after cleavage.

NHS-HCCA
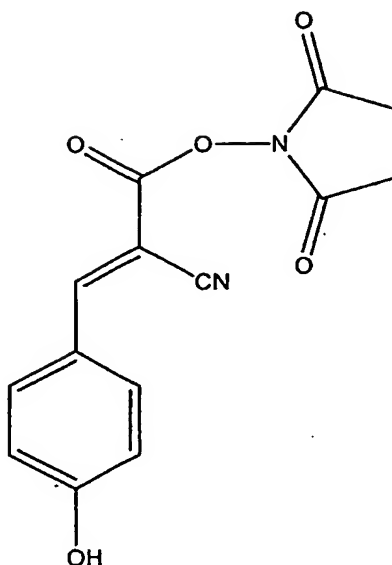
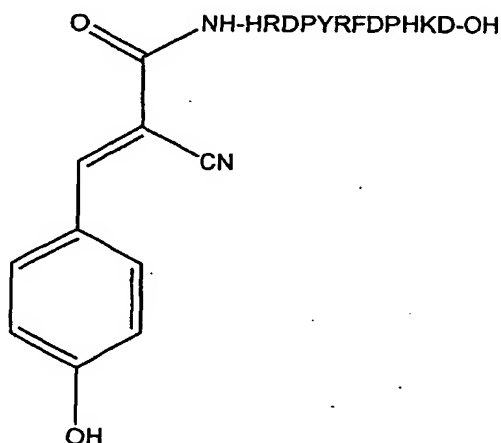| Molecular Weight = | 286.24 |
Exact Mass =	286.06
Molecular Formula =	$C_{14}H_{10}N_2O_5$
Molecular Composition =	C 58.7 %, H 3.5 %, N 9.8 %, O 28.0 %

Protocol for the labelling

The resin bound peptide was deprotected at the N-terminus following standard methods (piperidine in DMF) and reacted with an excess of the above reagent NHS-HCCA and with excess of a base (117 mg = 0.4 mol in 800 μl DMF with 1 eq. = 44.3 mg DIPEA). The mixture was incubated at room temperature for 3h.

Cleavage and work-up

After the labelling, the resin was washed and the peptide was cleaved off of the resin by incubation for 2 hours with the following scavenger mix: TFA:thioanisole:triethylsilane:water; 92.5 %:2.5 %:2.5 %:2.5 % respectively. The peptide was precipitated and washed with diethyl ether and lyophilised from tert-butanol/water (4:1) to yield a white powder.

Structure of the desired compound
NH-HRDPYRFDPHKD-COOH ·

Molecular weight: 1753.87 g/mol (average) / 1752.78 g/mol (monoisotopic)
Mono-isotopic composition: $C_{80}H_{104}N_{24}O_{22}$

Example 5 - Analysis of NHS-HCCA labelled peptide and comparison with unlabelled peptide

The product of the labelling reaction was analysed by HPLC (see Figure 2) and was found to comprise a mixture of labelled and unlabelled peptide. The labelled peptide comprises about 85 % of the mixture while the unlabelled peptide comprises about 15 % of the mixture. Analysis of the mixture by electrospray ionisation mass spectrometry does not show any improvement in the sensitivity of detection of the labelled peptide however analysis of the mixture by MALDI TOF MS (Figure 3) shows that the labelled

peptide, which is present as a smaller percentage of the mixture is detected with far greater sensitivity than the unlabelled peptide.

Example 6 - Reaction of NHS-L-HCCA with Resin-bound Peptides

The second active ester cinnamic acid mass tag (NHS-L-HCCA) comprising an additional six carbon chain linker, whose synthesis is described above, was attached to resin bound peptides according to the following procedures.
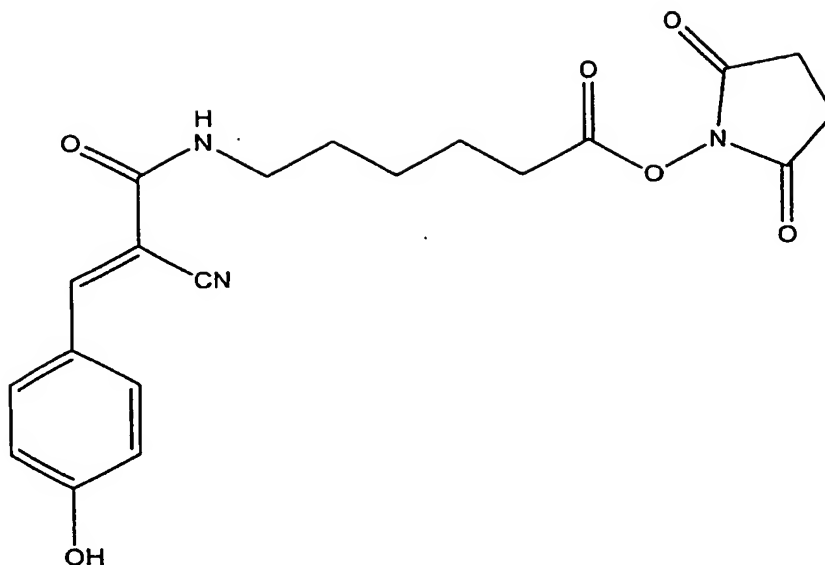
Peptides

The following peptide sequences were synthesised on a Wang type resin using standard Fmoc/tBu synthesis procedures:

HSRGARGHSHAHRG	(highly basic)	M: 1522.62
YDSGEGDESDAYEG	(highly acidic)	M: 1493.38
LGWSGFGWSFSYLG	(highly hydrophobic)`	M: 1563.75

(bound to a trityl type resin to yield a free acid after cleavage)

NHS-L-HCCA

Molecular Weight =	399.40
Exact Mass =	399.14
Molecular Formula =	$C_{20}H_{21}N_3O_6$
Molecular Composition =	C 60.14 %, H 5.30 %, N 10.52 %, O 24.04 %

Protocol for peptide labelling

The resin bound peptide was deprotected at the N-terminus following standard methods (piperidine in DMF) and reacted with an excess of the reagent NHS-L-HCCA and with an excess of a base (128mg = 0.4M in 800µl DMF with 1eq. = 44.3mg DIPEA). The mixture was incubated at room temperature for 3 hours.

Cleavage and work-up

After the labelling reaction, the resin was washed and the peptides were cleaved from the resin by incubation for 2 hours with the following scavenger mix: TFA 92.5 % / thioanisole; 2.5 % / triethylsilane; 2.5 % / water; 2.5 %. The peptides were precipitated

and washed with diethyl ether.   Finally, the peptides were lyophilised from tert-
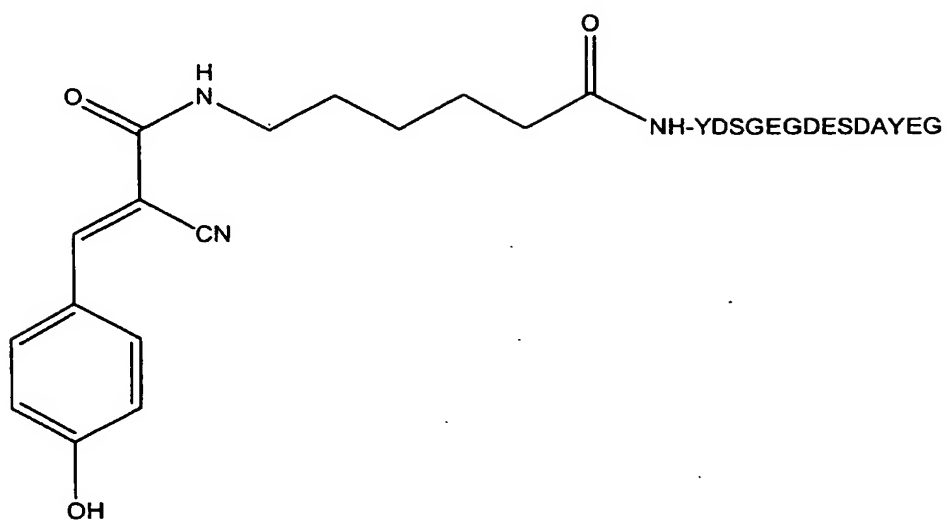butanol/water (4:1) to yield a white powder.

Structure of the desired compounds
NH-HSRGARGHSHAHRG-COOH
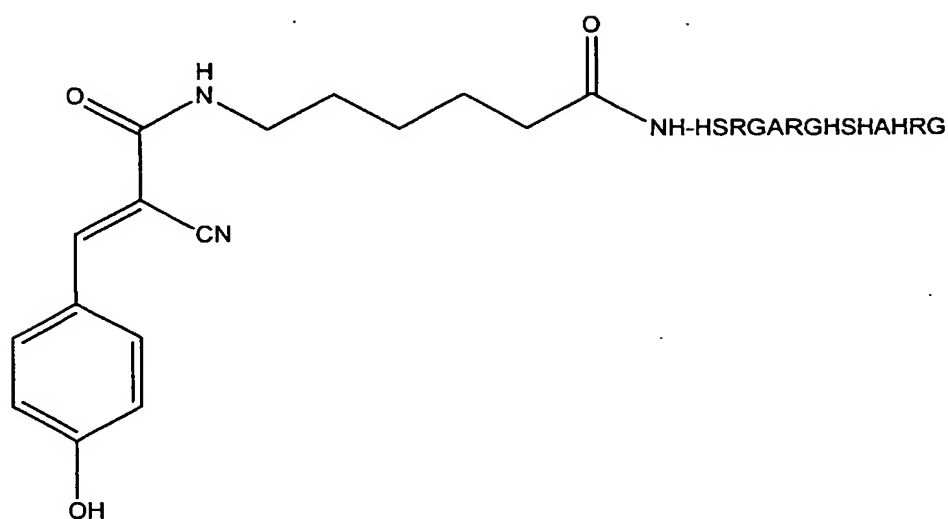
Molecular weight: 1806.94 g/mol (average) / 1805.87 g/mol (mono-isotopic)
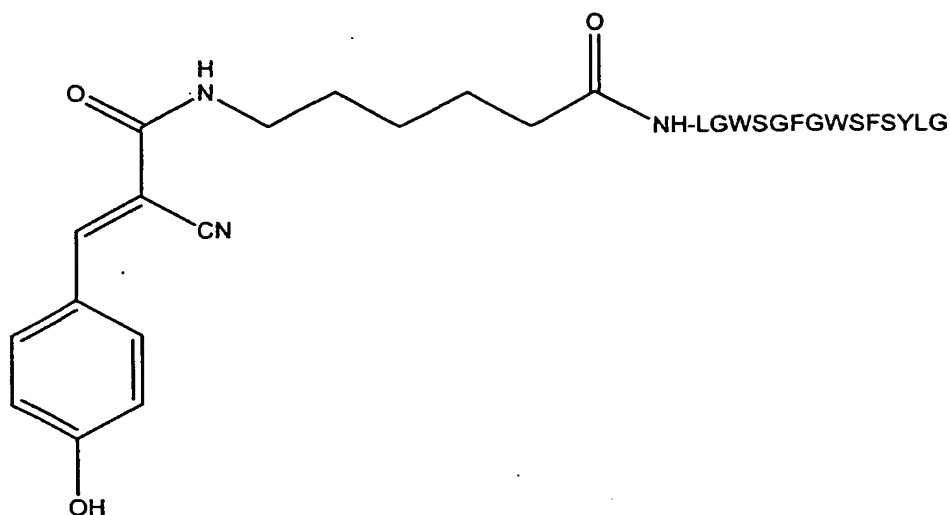Mono-isotopic composition: $C_{76}H_{111}N_{33}O_{20}$

NH-YDSGEGDESDAYEG-COOH

Molecular weight: 1777.70 g/mol (average) / 1776.63 g/mol (mono-isotopic)

Mono-isotopic composition: $C_{76}H_{96}N_{16}O_{34}$.

NH-LGWSGFGWSFSYLG-COOH

Molecular weight: 1848.06 g/mol (average) / 1846.84 g/mol (mono-isotopic)

Mono-isotopic composition: $C_{94}H_{114}N_{18}O_{22}$.

Example 6 - Analysis of NHS-L-HCCA labelled peptide and comparison with unlabelled peptide

The peptides were analysed by HPLC. The first peptide, HSRGARGHSHAHRG, was isolated pure as the reaction with the tag containing the linker went to completion. The labelled peptide was combined with unlabelled peptide to give a 50/50 mixture at a concentration of 1μmol/μl of each peptide. Analysis of the mixture by electrospray ionisation mass spectrometry does not show any improvement in the sensitivity of detection of the labelled peptide compared to the unlabelled peptide. However, 0.5μl of the mixture on a metal target analysed by MALDI TOF MS shows that the labelled peptide is detected with greater sensitivity than the unlabelled peptide. This indicates that the linker functionality does not reduce the effectiveness of the tag and can be used to improve the yield of the labelling reaction.

Example 7 - Reaction of NHS-L-HCCA with Beta-MSH Peptides

Matrix MT
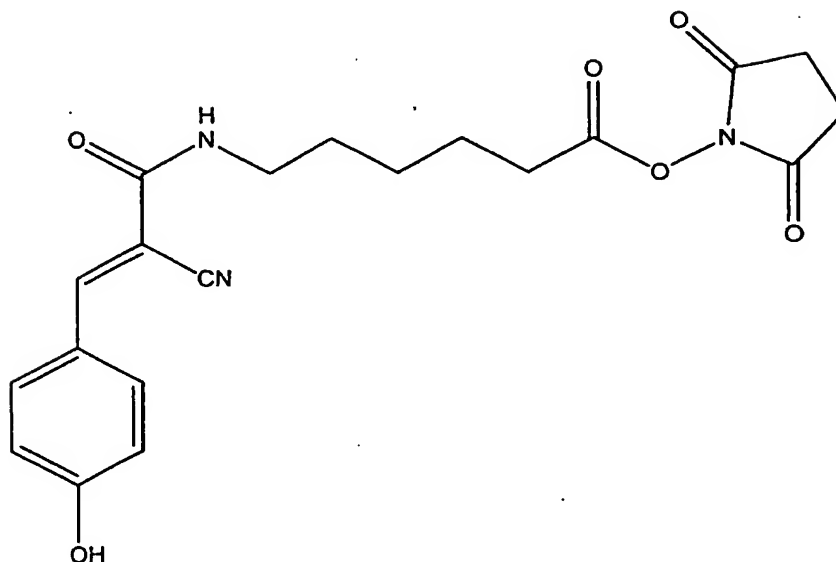
Molecular Formula of NHS-L-HCCA: $C_{20}H_{21}N_3O_6$

Molecular Weight: 399.41

Peptide labelling in solution

Protein: β-MSH (DEGPYKMEHFRWGSPPKD, M: 2175)

1 mg (0.46 µmol) peptide is dissolved in water/acetonitrile (250 µl, 90/10). 30 µg trypsin in borate buffer (100 µl, pH 8,0) are added to the peptide solution. The digestion is carried out for 18 h at 37°C.

2.5 mg (6.3 mmol) NHS-L-HCCA in 250 µL acetonitrile are added to 175 µl (1/2 of the digest solution) of the tryptic peptide solution. The labelling reaction is carried out for 5 h at RT and at pH 7.,5. The reaction is then quenched by adding 100 µl H₂O/acetonitrile (95/5) and 1 % TFA. The labelled peptide solution is then experimented in MALDI MS.

Example 8 - Comparison of spectra from NHS-L-HCCA labelled beta-MSH peptides with unlabeled beta-MSH peptides

Peptide mass fingerprints from beta-MSH

Tryptic digest of unlabeled beta-MSH gives rise to 3 fragments as shown in Table 2 below.

Table 2

m/z		Fragment Positions	Cleavage	Composition	
Isotopic Mass (Daltons)	Average Mass (Daltons)	Start	Finish	No. of reactive groups	Sequence
708.3204	708.7507	1	6	2	DEGPYK
719.3299	719.8458	7	11	2	MEHFR
786.3786	786.8682	12	18	2	WGSPPKD

Tryptic digest of labelled beta-MSH gives rise to 3 fragments as shown in Table 3 below.

Table 3

m/z	Fragment Positions	Cleavage	Composition	
Isotopic Mass (Daltons)	Start	Finish	No. of tagged reactive groups	Sequence
992.435	1	6	1	DEGPYK + 1 tag
1276.535	1	6	2	DEGPYK + 2 tags
1003.445	7	11	1	MEHFR + 1 tag
1287.560	7	11	2	MEHFR + 2 tags
1354.609	12	18	2	WGSPPKD + 2 tags

Various experiments were performed on the above labelled and unlabelled digests. A schematic of the labelling protocol for beta-MSH is shown in Figure 5a. Figure 5b shows the MALDI TOF mass spectrum of the unlabelled and undigested peptide.

Figure 6 shows spectra MALDI TOF for the unlabelled and labelled digests of beta-MSH. It can be seen that the 3 expected peptides for the unlabeled digest are present in the spectrum of the unlabeled peptides. The labelled peptide spectrum shows 4 different species. The peptide comprising amino acids 1 to 6 has 2 sites available for labelling; the alpha-amino group and the lysine epsilon amino group. Both of these appear to be fully labelled and only one species corresponding to the doubly labelled peptide appears in the spectrum. Similarly, the peptide comprising amino acids 12 to 18 has 2 sites available for labelling; the alpha-amino group and the lysine epsilon amino group and again both appear to be fully labelled and only one species corresponding to the doubly labelled peptide appears in the spectrum. The peptide comprising amino acids 7 to 11 should only label at the alpha-amino group but appears to have been labelled twice in the mass spectrum as 2 species corresponding to this peptide are detected in the spectrum of the labelled fragments. There is a minor side-reaction where the NHS-L-HCCA reacts with histidine giving rise to a second peak in the spectrum for this peptide.

The singly labelled peptide comprising amino acids 7 to 11 of beta-MSH appeared most strongly in the spectrum of the labelled protein. This peptide fragment was isolated by HPLC chromatography and solutions of this peptide were prepared. Figure 7 shows MALDI TOF mass spectra of this peptide mixed in various molar ratios with the digest of unlabelled beta-MSH. It can clearly be observed that the detected abundance of the labelled peptide is greater than the unlabelled peptides even at the lowest ratio of labelled to unlabelled peptides (5:95).

Figure 8 shows the results of a further experiment to demonstrate the enhancement in sensitivity provided by the tags of this invention. Figure 8 shows a number of MALDI TOF mass spectra for a serial dilution of a stock solution of 44 pmol of the labelled peptide comprising amino acids 7 to 11 of beta-MSH mixed with 180 pmol of digested and unlabeled beta-MSH. The first spectrum shows the MALDI TOF analysis of the stock solution. Both the labelled peptide and the unlabeled peptides can be seen in various dilutions of the stock solution (spectra not shown) until a 625-fold dilution is

reached, which is the second spectrum shown in Figure 8. Labelled and unlabelled peptides can still be seen at this dilution but noise can be seen in the low mass ranges of the spectrum. A further 5-fold dilution to a dilution of 3125-fold gives a spectrum in which the unlabeled peptides can no longer be detected but the labelled peptide is still detectable. The labelled peptide is still detectable in a further 5-fold dilution of the solution (15625-fold). The above results all indicate that there is a significant enhancement in the sensitivity of detection of peptides when covalently attached to a tag comprising a MALDI matrix.

Example 9 - Peptide Mass Fingerprinting experiments with proteins
A further set of experiments with whole proteins were carried out. The proteins bovine serum albumin (BSA) and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) were analysed individually.

Labelling of Tryptic Digests of BSA and GAPDH:
BSA (Probe A):   69,2 kDa / 60 * Lys / 26 * Arg
GAPDH (Probe B):   35,7 kDa / 26 * Lys / 10 * Arg

A stock solution of 2 µg/µl protein in borate buffer (50 mmol, pH 8) and urea/thiourea (100 mmol, 2/1) is freshly prepared. 20 µl (1 µg/µl) trypsin are added to 260 µl of protein stock solution. The enzymatic cleavage reaction is carried out for 16 h at 37°C, pH 8.0

160 µl of the tryptic peptide solution are labelled with 2.5 mg NHS-L-HCCA dissolved in 250 µl acetonitrile. After 5 hours labelling at 25°C, pH 7.8, the reaction is then quenched by adding 100 µl H_2O/acetonitrile (95/5) + 1 % TFA.

Example 10 - Comparison of spectra from NHS-HCCA labelled BSA peptides with unlabeled BSA peptides:
Figure 9 shows a typical MALDI TOF peptide mass fingerprint mass spectrum for BSA. The mass determined in this spectrum can be used to search a database of known and predicted mass spectra to identify the protein from its component tryptic peptide fragment

masses. Figure 10 shows the results of a search of the SWISS-PROT database, with some of the masses from the spectrum shown in Figure 10, using the MS-Fit program on the ProteinProspector database server. This tool is available on the world wide web and allows the identification of proteins with modified amino acids (Clauser K. R., Baker P. R. and Burlingame A. L., Analytical Chemistry, Vol. 71(14): 2871, "Role of accurate mass measurement (+/- 10 ppm) in protein identification strategies employing MS or MS/MS and database searching." (1999)). The modified amino acid masses are entered into the program along with a series of modified peptide masses. The output of the program is a list of proteins that contain peptides that match the masses submitted to the database. The matching peptides for each matching protein, identified by MS-Fit, can then be displayed to determine how well the peptides match the protein, which is shown in Figure 10. This analysis was performed with unmodified lysine.

Figure 11 shows the corresponding MALDI TOF peptide mass fingerprint mass spectrum for NHS-L-HCCA labelled BSA. Figure 12 shows the peptides that match BSA from a search of the SWISS-PROT database using the MS-Fit program, in which the appropriately modified lysine mass has been entered, along with peptide masses from the spectrum in Figure 11.

Figure 13 shows a typical MALDI TOF peptide mass fingerprint mass spectrum for GAPDH. The mass determined in this spectrum can be used to search a database of known and predicted mass spectra to identify the protein from its component tryptic peptide fragment masses. Figure 14 shows the results of a search of the SWISS-PROT database, with some of the masses from the spectrum shown in Figure 13, using the MS-Fit program, where unmodified lysine is searched for.

Figure 15 shows the corresponding MALDI TOF peptide mass fingerprint mass spectrum for NHS-L-HCCA labelled BSA. Figure 16 shows the peptides that match GAPDH from a search of the SWISS-PROT database using the MS-Fit program, in which the appropriately modified lysine mass has been entered, along with peptide masses from the spectrum in Figure 15.

Example 11 – preparation of exemplary tags

The following examples show the syntheses of further novel tags, shown in Figures 17a-17d, provided by this invention. These tags all include an ionisable functionality. Ionisable functionalities serve several useful purposes. Ionisable functionalities improve the solubility of the tags in aqueous solvents and buffers. Ionisable functionalities can act as affinity ligands allowing unreacted tag to be separated from labelled analytes using ion exchange resins. The sulphonic acid moiety has an affinity to anion exchange resins while the positively ionising groups all have an affinity for cation exchange resins. In addition, ionisable functionalities promote ionisation in the mass spectrometer. The tag shown in figure 17a comprises a sulphonic acid functionality. The tags in figures 17b and 17c comprise a guanidino functionality, while the tag in figure 17d comprises a tertiary amino functionality.

Synthesis of 6-[2-Cyano-3-(4-hydroxy-3-sulfonato-phenyl)-acryloylamino]-hexanoic acid-(2,5-dioxo-pyrrolidin-1-yl)-ester Sodium

The synthesis of the tag compound shown in Figure 17a is now described. The intermediates are numbered according to the scheme shown in Figure 18.
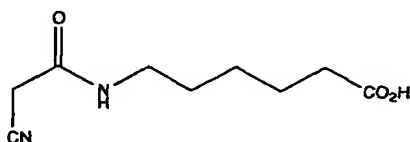
6-(2-Chloroacetylamino)-hexanoic acid (5)
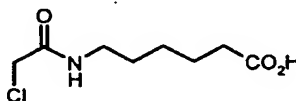
5

20 g (153 mMol) 6-Amino-hexanoic acid was mixed with 80 ml of 2N Sodium Hydroxide (NaOH). 18 ml (221 mMol) of Chloro-acetylchloride and 6N NaOH were added to the mixture at Room Temperature (RT). The pH of the reaction mixture was maintained between 10 and 11 during the addition of Chloro-acetylchloride and 6N NaOH by using a burette to control the addition. The mixture was stirred for 30 mins at

this constant pH. Ethyl acetate (EtOAc) was then added to the reaction mixture and the pH was adjusted to 2 with 2N Hydrochloric Acid (HCl). To work up the product, the EtOAc-layer was separated and the aqueous phase was extracted with EtOAc. The organic layers were dried and the solvent was evaporated. The residue was then re-crystallized from diisopropylether/EtOAc (1:1, v:v).

Yield: 25.3 g (80%); Mp 82°C
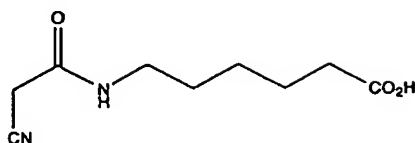
6-(2-Cyano-acetylamino)-hexanoic acid (1)

1

8.3 g (40 mMol) 6-(2-Chloro-acetylamino)-hexanoic acid 5 was dissolved with 2.8 g (20 Mol) K_2CO_3 in 25 ml water at RT. After having added 3.2 g (48 mMol) KCN, the reaction mixture was stirred for 17h at RT. The pH of the solution was then altered to 2 with 2N HCl and the product was extracted with EtOAc. After drying the product over sodium sulphate and evaporating the solvent, the product was purified by chromatography using ethyl acetate. The compound was then re-crystallized from EtOAc.

Yield: 6 g (76%); Mp 90°C

HPLC: 97% [LiChrospher 100, RP 18, (5µm); CH_3CN : (H_2O + 0.01M TBAS) = 40:60, flow 1 ml/Min.; 2.4 Min.]

^{1}H-NMR (d_6-DMSO) δ 1.23-1.50 (m, m, m, 6H, N-C-(CH$_2$)$_3$-C-CO); 2.18 (t, 2H, CH$_2$-CO$_2$); 3.05 (m, 2H, N-CH$_2$); 3.56 (s, 2H, NC-CH$_2$); 8.15 (t, 1H, NH); 11.94 (s, 1H, OH)

6-(2-Cyano-acetylamino)-hexanoic acid (1)

1

6.55 g (50 mMol) 6-Amino-hexanoic acid and 9.2 g (110 mMol) NaHCO₃ were dissolved in 80 ml water. A solution of 9.1 g Cyanoacetic acid-(2,5-dioxo-pyrrolidine-1-yl)-ester [*C. Bartolucci et al.,* **47**, 1367 (1992)] was added in portions to the mixture at RT. After stirring the reaction mixture for 16h at RT, the pH of the solution was altered to 2 with 2N HCl and the product was extracted with ethyl acetate. The organic layer was dried over sodium sulphate and the solvent was then evaporated. The compound was then re-crystallized from EtOAc.

Yield: 5 g (51%); Mp: 95°C

HPLC: >98% [LiChrospher 100, RP 18, (5μm); CH₃CN : (H₂O + 0.01M TBAS) = 40:60, flow 1 ml/Min.; 2.4 Min.]

¹H-NMR (*d₆*-DMSO) δ 1.23-1.50 (m, m, m, 6H, N-C-(CH₂)₃-C-CO); 2.18 (t, 2H, CH₂-CO₂); 3.05 (m, 2H, N-CH₂); 3.56 (s, 2H, NC-CH₂); 8.15 (t, 1H, NH); 11.94 (s, 1H, OH)

Sodium 3-Formyl-6 hydroxy-phenyl-sulfonate (7)

7

20 g (164 mMol) 4-Hydroxybenzaldehyde was dissolved in 100 mM conc. H_2SO_4 and the solution was stirred for 20h at 80°C. The cooled solution was then poured onto 350g ice. After adding 60 g Sodium Chloride (NaCl), a crystallized colourless product formed after a short time. After cooling to 0°C, the product was filtered off and was washed twice with 50 ml saturated NaCl solution. The solid residue was then heated in 150 ml saturated NaCl solution, cooled down and filtered off. The residue was washed again twice with 25 ml saturated NaCl solution and twice with 15 ml ice-cold water. The sodium salt was obtained by slurrying the product in 150 ml water and by neutralisation the solution to pH 7.2 with 2N NaOH. At this point, traces of starting material in the solution (aldehyde adduct) could be extracted with ethyl acetate. The aqueous layer was treated with A-Kohle, filtered off and the solution was evaporated under vacuum. The dried solid residue was treated with acetone and filtered off.
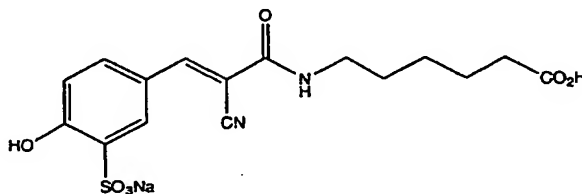
Yield: 30.5 g (83%)

$R_F = 0.48$ (EtOAc/AcOH = 2:1)

HPLC: >98% [LiChrospher 100, RP 18, (5μm) Merck# 50377; CH_3CN : (H_2O + 0.01M TBAS) = 40:60, flow 1 ml/Min.; 5.2 Min.]

^{1}H-NMR (d_6-DMSO) δ 6.53 (d, 1H, 5-H-Ph); 7.50 (m, 1H, 4-H-Ph); 7.92 (d, 1H, 2-H-Ph); 9.50 (s, 1H, OH)

Sodium 6-[2-Cyano-3-(4-hydroxy-3-sulfonato-phenyl)-acryloylamino]-hexanoic acid (2)


2

17.85 g (90 mMol) 6-(2-Cyano-acetylamino)-hexanoic acid (1) and 17.92 g (80 mMol) Sodium 3-Formyl-6 hydroxy-phenyl-sulfonate (7) were stirred in 160 ml Pyridine and 1.6 ml Piperidine for 3 days at 65°C. The reaction mixture was diluted with 200 ml Acetonitrile and the residue was filtered off and washed with Acetonitrile and Acetone. The solid residue was heated in 150 ml Acetonitrile for 1h, cooled down and filtered off.

Yield:28 g (86%)

HPLC: 93% [LiChrospher 100, RP 18, (5µm) Merck# 50377; CH_3CN : (H_2O + 0.01M TBAS) = 40:60, flow 1 ml/Min.; 6.3 Min.]

^{1}H-NMR (D_2O) δ 1.29-1.36 u. 1.53-1.60 (m, m, 6H, N-C-$(CH_2)_3$-C-CO); 2.14-2.19 (m, 2H, CH_2-CO_2); 3.25-3.28 (m, 2H, N-CH_2); 6.73 (d, 1H, 5-H-Ph); 7.80 (m, 1H, 6-H-Ph); 8.30 (d, 1H, 2-H-Ph); 7.92 (s, 1H, CH=C-CN)

Sodium   6-[2-Cyano-3-(4-hydroxy-3-sulfonato-phenyl)-acryloylamino]-hexanoic   acid-(2,5-dioxo-pyrrolidine-1-yl)-ester (3)
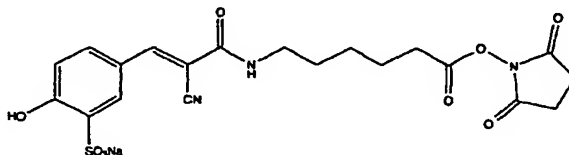
3

9.2 g (80 mMol) N-Hydroxy-succinimide was melt at 90-100°C (water bath temperature). 4.04 g Sodium (10 mMol) 6-[2-Cyano-3-(4-hydroxy-3-sulfonato-phenyl)-acryloylamino]-hexanoic acid 2 was added in portions to the molten residue and the mixture was stirred to get a homogenous phase. After adding 15 mg DMAP to the reaction mixture, a solution of 4.12 g (20 mMol) Dicyclohexylcarbodiimide dissolved in 50 ml Acetonitrile was added drop-wise to the reaction mixture and the solution obtained was heated under reflux for 1h. Then, a further 100 ml of Acetonitrile was added to the solution. The solid

residue was filtered off and the filtrate was evaporated. The residue recovered from the filtrate was dissolved in acetone and separated from any insoluble residue. The solution was reduced to ca. 50 ml and the product was precipitated by adding 250 ml EtOAc. The precipitated product was dissolved in water and the aqueous layer was extracted several times with EtOAc. The aqueous phase was then lyophilised.

Yield: 1.42 g (28%)

HPLC: >90% [Lichrosorb RP 18, (5μm) Merck# 50333; CH_3CN : (H_2O + 0.01M TBAS) = 40:60, flow 1 ml/Min.; 10.3 Min.]

^{1}H-NMR (D_2O) δ 1.39-1.67 (m, m, m, 6H, N-C-$(CH_2)_3$-C-CO); 2.69 (t, 2H, CH_2-CO_2); 2.80 (s, 4H, OSu); 3.18-3.20 (m, 2H, N-CH_2); 6.97 (d, 1H, 5-H-Ph); 7.92 (m, 1H, 6-H-Ph); 8.13 (d, 1H, 2-H-Ph); 8.03 (s, 1H, CH=C-CN); 8.31 (t, 1H, NH); 11.22 (s, 1H, OH)

Synthesis of N^α-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg$^{\omega\omega'}$(Boc$_2$)-2,5-dioxo-pyrrolidine-1-yl ester

The synthesis of the tag compound shown in Figure 17b is now described. The intermediates are numbered according to the scheme shown in Figure 19.

N^α-(2-Cyano-acetyl)-Arg$^{\omega\omega'}$(Boc2)-OH (2)

2
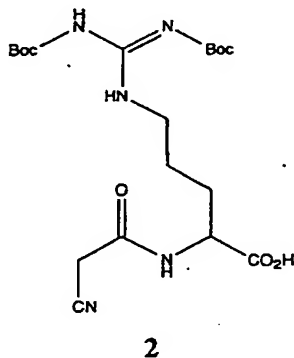
4 g (5 mMol) Cu[Arg$^{\omega\omega'}$(Boc$_2$)]$_2$ [*M. Bernatowicz et al.*, Synth. Commun. **23**, 3055 (1993)], 2.74 g (6 mMol) EDTA·4Na·H$_2$O and 1.97 g (23.5 mMol) NaHCO$_3$ were dissolved in 19 ml water. A solution of 2.18 g (11.96 mMol) 2-Cyano-acetic acid-OSu-ester dissolved in 46 ml Acetone was added drop-wise to the reaction mixture at RT. The mixture was then stirred for 16h. The acetone layer was evaporated and the pH of the aqueous layer was adjusted to 3 with a 5% KHSO$_4$-solution. The product was extracted with EtOAc. After having dried the organic layer and evaporated the solvent, the product was purified by chromatography using CH$_2$Cl$_2$/CH$_3$OH (10:1, v:v)

Yield: 2.2 g (50%)

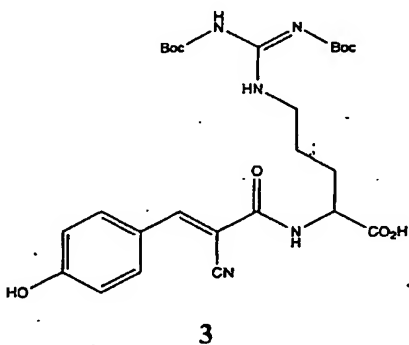HPLC: 96% [LiChrospher 100 RP 18, (5µm) Merck# 50377; CH$_3$CN : (H$_2$O + 0.01M TBAS) = 90:10, flow 1 ml/Min.; 2.5 Min.]

N$^\alpha$-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg$^{\omega\omega'}$(Boc$_2$)-OH (3)

3

19.5 g (44 mMol) N$^\alpha$-(2-Cyano-acetyl)-Arg$^{\omega\omega'}$(Boc$_2$)-OH **2** and 5.37 g (4 mMol) 4-Hydroxy-benzaldehyde was added to 60 ml Pyridine with 0.9 ml Piperidine. The mixture was heated to 50 °C for 2h and was then stirred for 16h at RT. Pyridine was evaporated under vacuum and the pH of the solution obtained was altered to 3 with a 5% KHSO$_4$ solution. After extracting the residue with EtOAc and drying the organic layer over

MgSO$_4$, the solvent was evaporated. The product was purified by chromatography using CH$_2$Cl$_2$/CH$_3$OH (100:3, v:v).

Yield: 14.2 g (59%)

HPLC: >98% [LiChrospher 100 RP 18, (5µm) Merck# 50377; CH$_3$CN : (H$_2$O + 0.01M TBAS) = 90:10, flow 1 ml/Min.; 2.6 Min.]

^{1}H-NMR (d_6-DMSO) δ 1.37 u. 1.45 (s, s, 18H, 2x t-Bu); 1.45-1.88 (m, 4H); 3.32 (m, 2H, N-CH$_2$); 4.31 (m, 1H, N-CH); 6.94 u. 7.88 (m, m, 4H, Ph); 8.06 (s, 1H, CH=C-CN); 8.31, 8.45, ~10.4, 11.5 u. 12.6 (5H, 3x NH, 2x OH)

N$^\alpha$-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg$^{\omega\omega'}$(Boc$_2$)-2,5-dioxo-pyrrolidine-1-yl ester (4)

4
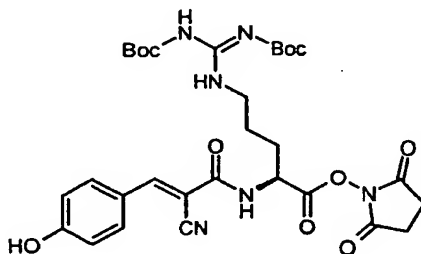
2.71 g (5 mMol) N$^\alpha$-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg$^{\omega\omega'}$(Boc$_2$)-OH 3 and 0.58 g (5 mMol) N-Hydroxy-succinimide were dissolved in 50 ml CH$_2$Cl$_2$. 1.03 g (5 mMol) Dicyclohexyl-carbodiimide was added to the reaction mixture and the solution was stirred for 20h at RT. The precipitate was filtered off and the filtrate was evaporated. The residue obtained was dissolved in EtOAc. The EtOAc layer was washed twice with NaHCO$_3$-solution, twice with 5% Citric acid and twice with saturated NaCl-solution, dried over MgSO$_4$ and the solvent was then evaporated. The remaining solid foam was dissolved in ca. 5 ml EtOAc and ca. 50 ml Diethylether was carefully added to this

solution until the solution became turbid. A-Kohle was then mixed to the mixture, stirred and filtered off. The filtrate was evaporated and the remaining residue was treated with Diisopropylether and then filtered off.

Yield: 1.58 g (50%)

^{1}H-NMR (CDCl$_3$) δ 1.32 u. 1.43 (s, s, 18H, 2x t-Bu); 1.57-2.04 (m, 4H); 2.78 (s, 4H, O-Su); 3.25-3.67 (m, 2H, N-CH$_2$); 4.88 (m, 1H, N-CH); 6.88 u. 7.76 (m, m, 4H, Ph); 8.04 (s, 1H, CH=C-CN); 7.21, 8.49, ~8.75, 11.45 (4H, 3x NH, OH)
MS: 643 (M+1)

Synthesis of N^α-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg-$^{\omega\omega'}$(Boc$_2$)-N-(6-amino-hexanoic acid-OSu-ester)

The synthesis of the tag compound shown in Figure 17c is now described. The intermediates are numbered according to the scheme shown in Figure 20.

N^α-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg-$^{\omega\omega'}$(Boc$_2$)-N-(6-amino-hexanoic acid) (2)

2
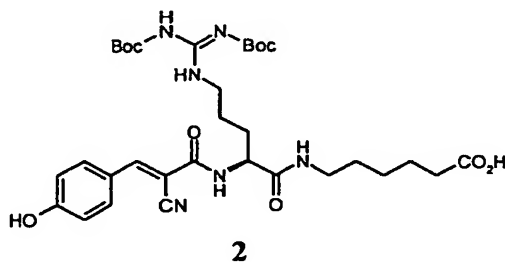
5.42 g (10 mMol) N^α-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg-$^{\omega\omega'}$(Boc$_2$)-OH (1) and 1.15 g (10 mMol) N-Hydroxy-succinimide were dissolved in 100 mL Dichloromethane. 2.06 g (10 mMol) Dicyclohexyl-carbodiimide was added to the solution and the reaction mixture was stirred for 20h at RT. The precipitate was filtered off and the filtrate was evaporated. The crude active ester product obtained from (1) was then dissolved in 45 ml

THF. An aqueous solution of 1.31 g (10 mMol) 6-Amino-hexanoic acid and 0.84 g (10 mMol) $NaHCO_3$ was added to the reaction mixture. After having stirred the reaction mixture for 20h at RT, the pH of the solution was altered to 3 with a 2N HCl solution and the product was extracted with EtOAc. The organic layer was then dried and evaporated. The residue was purified by chromatography using EtOAc/Diisopropylether (1:1,v:v)

Yield: 2.6 g (40%)

HPLC: >98% [Lichrosorb RP 18, (5µm) Merck# 50333; CH_3CN : (H_2O + 0.01M TBAS) = 55:45, flow 1 ml/Min.; 4.1 Min.]

^{1}H-NMR ($CDCl_3$) δ 1.43 u. 1.48 (s, s, 18H, 2x t-Bu); 1.30-1.73 (m, 10H); 1.74-1.85 (m, 1H); 1.85-1.97 (m, 1H); 2.34 (m, 2H); 3.15-3.39 (m, 2H); 3.45 (m, 2H); 4.51 (m, 1H); 6.92 u. 7.76 (m, m, 4H, Ph); 8.0 (s, 1H, CH=C-CN); 7.03, 7.26, 8.55, 9.5 (4H, 3x NH, OH)

N^α-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg-$\omega\omega^\epsilon$(Boc$_2$)-N-(6-amino-hexanoic acid-OSu-ester) (3)

3

2.63 g (4 mMol) N^α-[2-Cyano-3-(4-hydroxyphenyl)-acryloyl]-Arg-$\omega\omega^\epsilon$(Boc$_2$)-N-(6-amino-hexanoic acid) (2) and 0.46 g (4 mMol) N-Hydroxy-succinimide were dissolved in 50 ml CH_2Cl_2. Then, 0.91 g (4.4 mMol) Dicyclohexyl-carbodiimide was added to the solution and the reaction mixture was stirred for 20h at RT. The precipitate was filtered

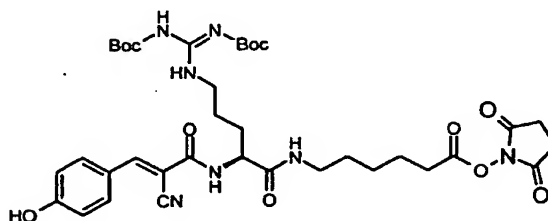off and the filtrate was evaporated. The residue obtained was then dissolved in EtOAc and the organic solution was washed with NaHCO3 solution and water. After having dried and evaporated the organic layer, the residue was rapidly purified by chromatography using a short silica gel column and EtOAc under modest pressure.

Yield: 1.53 g (50%)

RF = 0.56 (EtOAc)

HPLC: 95% [Lichrosorb RP 18, (5μm) Merck# 50333; CH₃CN : (H₂O + 0.01M TBAS) = 55:45, flow 1 ml/Min.; 6.1 Min.]

^{1}H-NMR (CDCl₃) δ 1.45 u. 1.49 (s, s, 18H, 2x t-Bu); 1.40-1.98 (m, 11H); 2.6 (t, 2H); 2.85 (s, 4H, OSu); 3.24-3.37 (m, 2H); 3.38-3.57 (m, 2H); 4.54 (m, 1H); 6.92 and 7.77 (m, m, 4H, Ph); 8.01 (s, 1H, CH=C-CN); 6.85, 7.09, 8.53, 11.45 (4H, 3x NH, OH)

Synthesis of 4-[2-Cyano-3-(4-hydroxy-phenyl)-acryloyl]-1-[5-(2,5-dioxo-pyrrolidine-1-yloxycarbonyl)-pentyl]-piperazine-1-ium hydrochloride

The synthesis of the tag compound shown in Figure 17d is now described. The intermediates are numbered according to the scheme shown in Figure 21.

4-Boc-1-(5-ethoxycarbonyl-pentyl)-piperazine (2)

2
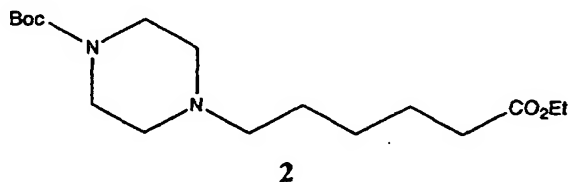
24.3 g (90 mMol) 6-Iodohexanoic acid-ethylester and 16.76 g (90 mMol) 1-Boc-piperazine 1 were dissolved in 75 ml THF and 16.95 ml (99 mMol) Diisopropyl-ethyl-amine was added to the solution. The reaction mixture was heated under reflux for 6 h.

The solvent was then evaporated under vacuum. The residue was dissolved in EtOAc and the solution obtained was washed 3 times with a NaHCO₃ solution and once with water. After having dried the organic layer over MgSO₄ and evaporated the solvent, the remaining oil was purified by chromatography using EtOAc.

Yield: 27.6 g (93%)

^{1}H-NMR (CDCl3) δ 1.25 (t, 3H, O-C-CH₃); 1.3-1.38 (m, 2H); 1.45 (s, 9H, t-Bu); 1.48-1.55 (m, 2H); 1.6-1.68 (m, 2H); 2.27-2.4 (m, 8H, 3x C-N-CH₂, CH₂-CO); 3.42 (t, 4H, 2x CO-N-CH₂); 4.12 (q, 2H, O-CH₂)

6-(Piperazine-1-yl)-hexanoic acid-ethylester (3)

3
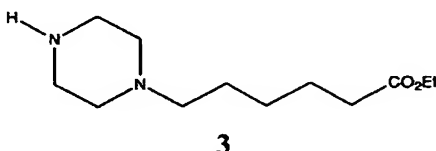
26.3 g (80 mMol) 4-Boc-1-(5-ethoxycarbonyl-pentyl)-piperazine (2) was dissolved in 150 ml 2N HCl and the solution was distilled using a rotary evaporator at 50°C under vacuum. The pH of the residue was altered to 10 with a 15 % NaOH solution and the product was extracted with EtOAc. The organic layer was dried over MgSO₄ and evaporated.

Yield: 2.2 g (66%)

HPLC >98% [Lichrosorb RP 18 (5µm) Merck# 50333; Acetonitrile/(H₂O + 0.01M TBAS) = 25:75; flow 1 ml/Min.; 6.3 Min.]

4-(2-Chloroacetyl)-1-(5-ethoxycarbonyl-pentyl)-piperazine (4)
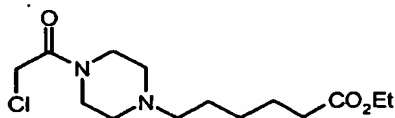
4

12.2 g (53 mMol) 6-(Piperazine-1-yl)-hexanoic acid ethylester **3** and 7.35 ml (53 mMol) TEA were dissolved in 140 ml CH_2Cl_2. After having added 4.22 ml (53 mMol) Chloro-acetylchloride drop-wise to the solution at 0°C, the reaction mixture was stirred for 2h at RT. The solution was washed twice with a $NaHCO_3$-solution and 1 time with water. After having dried the organic layer over $MgSO_4$ and evaporated the solvent, the remaining oil was purified by chromatography using EtOAc/CH_3OH (10:1, v:v)

Yield: 10.3 g (67%)

$R_F = 0.44$ (EtOAc/CH_3OH = 5:1)

HPLC 91% [Lichrosorb RP 18 (5µm) Merck# 50333; Acetonitrile/(H_2O + 0.01M TBAS) = 25:75; flow 1 ml/Min.; 2.1 Min.]

At this stage, the compound is pure enough for the synthesis of compound (**5**).

4-(2-Cyanoacetyl)-1-(5-ethoxycarbonyl-pentyl)-piperazine (5)
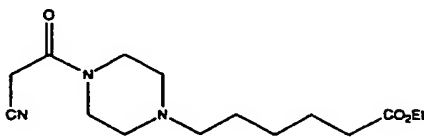
5

10.3 g (36 mMol) 4-(2-Chloroacetyl)-1-(5-ethoxycarbonyl-pentyl)-piperazine **(4)** and 2.76 g (42 mMol) KCN were dissolved in 50 ml DMSO and the mixture was stirred for 3h at RT. After cooling down the solution, the mixture was poured into 300 ml water and the product was extracted with EtOAc. The organic layer was washed twice with saturated NaCl solution, dried over MgSO$_4$ and then the solvent was evaporated. The residue was purified by chromatography using EtOAc/CH$_3$OH (10:1,v:v)

Yield: 5.2 g (53%)

HPLC >98% [Lichrosorb RP 18 (5μm) Merck# 50333; Acetonitrile/(H$_2$O + 0.01M TBAS) = 25:75; flow 1 ml/Min.; 2.0 Min.]

^{1}H-NMR (CDCl3) δ 1.25 (t, 3H, O-C-CH$_3$); 1.31-1.39, 1.46-1.54, 1.6-1.68 (m, m, m, 6H, N-C-(CH$_2$)$_3$-C-CO); 2.3, 2.36, 2.42 u. 2.49 (t, t, t, t, 8H, 3x C-N-CH$_2$, CH$_2$-CO); 3.45 u. 3.62 (t, t, 4H, 2x CO-N-CH$_2$); 3.53 (s, 2H, NC-CH$_2$); 4.12 (q, 2H, O-CH$_2$)

4-[2-Cyano-3-(4-hydroxy-phenyl)-acryloyl]-1-(5-ethoxycarbonyl-pentyl)-piperazine(6)
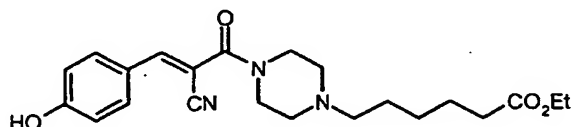
6

5.15 g (18.4 mMol) 4-(2-Cyano-acetyl)-1-(5-ethoxycarbonyl-pentyl)-piperazine **5** and 2.25 g (18.4 mMol) 4-Hydroxy benzaldehyde was dissolved in 30 mL Pyridine. After adding 0.33 ml Piperidine to the solution, the reaction mixture was stirred for 3h at 55°C and 20h at RT. Pyridine was then evaporated under vacuum and the residue was dissolved in EtOAc. The organic solution was washed 3 times with a saturated NaCl-solution, dried over MgSO$_4$ and the solvent was evaporated. The remaining product was purified by chromatography using EtOAc/CH$_3$OH (10:1, v:v)

Yield: 5.8 g (79%)

HPLC >98% [Lichrosorb RP 18 (5μm) Merck# 50333; Acetonitrile/(H$_2$O + 0.01M TBAS) = 25:75; flow 1 ml/Min.; 3.0 Min.]

^{1}H-NMR (d_6-DMSO) δ 1.17 (t, 3H, O-C-CH$_3$); 1.23-1.32, 1.38-1.47, 1.49-1.57 (m, m, m, 6H, N-C-(CH$_2$)$_3$-C-CO); 2.24-2.31. 2.38, 2.42 u. 2.49 (m, t, 8H, 3x C-N-CH$_2$, CH$_2$-CO); 3.54 (t, 4H, 2x CO-N-CH$_2$); 4.04 (q, 2H, O-CH$_2$); 6.91 u. 7.83 (m, m, 4H, Ph); 7.62 (s, 1H, CH=C-CN); 10.47 (br.s, 1H, OH)

4-[2-Cyano-3-(4-hydroxy-phenyl)-acryloyl]-1-(5-hydroxycarbonyl-pentyl)-piperazine-1-ium; hydrochloride (7)

7
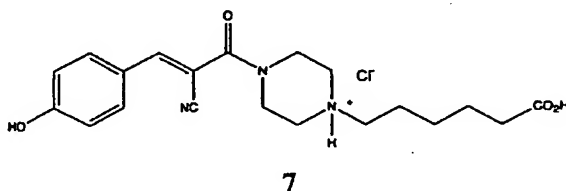
5.79 g (14.5 mMol) 4-[2-Cyano-3-(4-hydroxy-phenyl)-acryloyl]-1-(5-ethoxycarbonyl-pentyl)-piperazine (6) was dissolved in 25 ml Methanol. 20 ml (40 mMol) 2N NaOH was added to the solution at RT and the reaction mixture was stirred for 2h at RT. The pH of the solution was then altered to 4.2 with 2N HCl and Methanol was distilled under vacuum. It remained an aqueous phase with an oily layer which re-crystallised after a short time. The product was filtered off and washed with water and acetone.

Yield: 4.5 g (76%)

HPLC 94% [Lichrosorb RP 18 (5μm) Merck# 50333; Acetonitrile/(H$_2$O + 0.01M TBAS) = 20:80; flow 1 ml/Min.; 2.3 Min.]

^{1}H-NMR (d_6-DMSO) δ 1.23-1.35, 1.46-1.56, 1.65-1.78 (m, m, m, 6H, N-C-(CH$_2$)$_3$-C-CO); 2.23 (t, 2H, CH$_2$-CO); 3.05 (m,4H, 2x CO-N-CH$_2$); 3.5 (m, 4H, 2x N$^+$-CH$_2$-C-N); 4.25 (m, 2H, N$^+$-CH$_2$); 6.95 u. 7.86 (m, m, 4H, Ph); 7.71 (s, 1H, CH=C-CN); 10.66 (s, 1H, $^+$NH); 11.34 and 12.04 (br.s, br,s, 2H, 2x OH)

4-[2-Cyano-3-(4-hydroxy-phenyl)-acryloyl]-1-[5-(2,5-dioxo-pyrrolidine-1-yloxycarbonyl)-pentyl]-piperazine-1-ium hydrochloride (8)
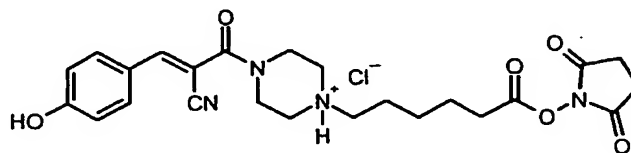
8

1.86 g (5 mMol) 4-[2-Cyano-3-(4-hydroxy-phenyl)-acryloyl]-1-(5-hydroxycarbonyl-pentyl)-piperazine-1-ium hydrochloride 7 and 0.64 g (5.5 mMol) N-Hydroxy-succinimide were dissolved in 25 ml DMF. 2.06 g (10 mMol) Dicyclohexyl-carbodiimide was added to the solution and the reaction mixture was stirred for 20h at RT. The precipitate was filtered off and the filtrate was mixed to 200 ml Diisopropylether. At this point, an oil formed. After having cooled down the mixture to -20°C, the residue got very viscous and a clear liquid could be removed. After having washed the residue twice with Diisopropylether, the oil was dissolved in Acetonitrile. The solution was filtered and the filtrate was then evaporated. The remaining solid foam was treated with EtOAc and filtered off.

Yield: 2.03 g (81%)

HPLC 97% [Lichrosorb RP 18 (5μm) Merck# 50333; Acetonitrile/(H$_2$O + 0.01M TBAS) = 15:85; flow 1 ml/Min.; 6.4 Min.]

^{1}H-NMR (d_6-DMSO) δ 1.35-1.47, 1.62-1.72, 1.72-1.85 (m, m, m, 6H, N-C-(CH$_2$)$_3$-C-CO); 2.67-2.75 (m, 2H, CH$_2$-CO); 2.83 (s, 4H, O-Su); 3.07 (m,4H, 2x CO-N-CH$_2$); 3.45-3.6 (m, 4H, 2x N$^+$-CH$_2$-C-N); 4.27 (m, 2H, N$^+$-CH$_2$); 6.97 and 7.87 (m, m, 4H, Ph); 7.72 (s, 1H, CH=C-CN); 10.69 u. 11.52 (s, s, 2H, $^+$NH, OH)

CLAIMS:

1.   A method for characterising an analyte by matrix assisted laser desorption ionisation (MALDI) mass spectrometry, which method comprises:

    (a)   labelling the analyte with a light-absorbing label that absorbs light at a pre-determined frequency, to form a labelled analyte;

    (b)   embedding the labelled analyte in a matrix formed from at least one compound that absorbs light, to form an embedded labelled analyte;

    (c)   desorbing the embedded labelled analyte by exposing it to light having the pre-determined frequency, to form a desorbed analyte; and

    (d)   detecting the desorbed analyte by mass spectrometry to characterise the analyte.

2.   A method according to claim 1, wherein the desorbed analyte is directly detected by mass spectrometry.

3.   A method according to claim 1, in which the desorbed analyte is indirectly detected by mass spectrometry, wherein the analyte is additionally labelled with a mass label relatable to the analyte, and wherein the mass label is cleaved from the desorbed analyte and detected by mass spectrometry to characterise the analyte.

4.   A method according to any preceding claim, wherein the light to which the embedded labelled analyte is exposed is laser light.

5.   A method according to any preceding claim, wherein the compound forming the matrix absorbs light at the same frequency as the light-absorbing label.

6.   A method according to any preceding claim, wherein the matrix and the light-absorbing label are formed from the same compound.

7.   A method according to any preceding claim, wherein the matrix is a solid matrix or a liquid matrix.

8.   A method according to claim 7, wherein the matrix is a liquid matrix comprising nitrobenzyl alcohol.

9.   A method according to any preceding claim, wherein the matrix comprises an acid matrix or a basic matrix.

10.   A method according to claim 9, wherein the matrix comprises a compound selected from 3-hydroxypicolinic acid, 2,5-dihydroxybenzoic acid and 4-hydroxy-alpha-cyanocinnamic acid.

11.   A method according to any preceding claim, wherein the light-absorbing label is formed from a dye.

12.   A method according to claim 11, wherein the dye is a non-fluorescent dye.

13.   A method according to claim 11 or claim 12, wherein the dye comprises 4-dimethylaminoazobenzine-4'-sulphonyl chloride (DABSYL chloride), 3-hydroxypicolinic acid, 2,5-dihydroxybenzoic acid and 4-hydroxy-alpha-cyanocinnamic acid.

14.   A method according to any preceding claim, wherein the analyte comprises one or more compounds selected from a protein, a polypeptide, a peptide, a peptide fragment and an amino acid.

15.   A method for characterising a polypeptide, which method comprises the steps of:

    (a)   optionally reducing cysteine disulphide bridges in the polypeptide to form free thiols, and capping the free thiols;

(b)   cleaving the polypeptide with a sequence specific cleavage reagent to form peptide fragments;

(c)   optionally deactivating the cleavage reagent;

(d)   capping one or more ε-amino groups that are present with a lysine reactive agent;

(e)   analysing peptide fragments according to a method as defined in any of claims 1-14 to form a mass fingerprint for the polypeptide; and

(f)   determining the identity of the polypeptide from the mass fingerprint.

16.   A method for characterising a population of polypeptides, which method comprises the steps of:

(h)   optionally reducing cysteine disulphide bridges in one or more polypeptides to form free thiols, and capping the free thiols;

(i)   separating one or more polypeptides from the population;

(j)   cleaving one or more polypeptides with a sequence specific cleavage reagent to form peptide fragments;

(k)   optionally deactivating the cleavage reagent;

(l)   capping one or more ε-amino groups that are present with a lysine reactive agent;

(m)   analysing peptide fragments according to a method as defined in any of claims 1-14 to form a mass fingerprint for one or more polypeptides; and

(n)   determining the identity of one or more polypeptides from the mass fingerprint.

17.   A method for comparing a plurality of samples, each sample comprising one or more polypeptides, which method comprises the steps of:

(h)   optionally reducing cysteine disulphide bridges and capping the free thiols in one or more polypeptides from the samples;

(i)   separating one or more polypeptides from each of the samples;

(j)   cleaving the polypeptides with a sequence specific cleavage reagent to form peptide fragments;

(k)   optionally deactivating the cleavage reagent;

(l)   capping one or more ε-amino groups that are present with a lysine reactive agent;

(m)   analysing peptide fragments according to a method as defined in any of claims 1-14 to form a mass fingerprint for one or more polypeptides from the samples; and

(n)   determining the identity of one or more polypeptides in the samples from one or more mass fingerprints.

18.   A method according to any of claims 15-17, wherein the lysine-reactive agent is a labelled lysine-reactive agent.

19.   A method according to claim 17, for comparing a plurality of samples, each sample comprising one or more polypeptides, which method comprises the steps of:

(a)   optionally reducing cysteine disulphide bridges and capping the free thiols in one or more polypeptides from the samples;

(b)   capping one or more ε-amino groups that are present in each sample with a labelled lysine reactive agent;

(c)   pooling the samples;

(d)   separating one or more polypeptides from the pooled samples;

(e)   cleaving the polypeptides with a sequence specific cleavage reagent to form peptide fragments;

(f)   optionally deactivating the cleavage reagent;

(g)   analysing peptide fragments according to a method as defined in any of claims 1-14 to form a mass fingerprint for one or more polypeptides from the samples; and

(h)   determining the identity of one or more polypeptides in the samples from one or more mass fingerprints.

wherein the same label is employed for polypeptides or peptides from the same sample, and different labels are employed for polypeptides or peptides from different samples, such that the sample from which a polypeptide or peptide originates can be determined from its label.

20.   A method according to any of claims 15-19, wherein the sequence specific cleavage agent cleaves the one or more polypeptides on the C-terminal side of a lysine residue.

21.   A method according to any of claims 15-20, wherein the specific cleavage reagent comprises Lys-C or Trypsin.

22.   A method according to any of claims 15-21, wherein the peptide fragments having capped ε-amino groups are removed by affinity capture, and wherein the lysine reactive agent comprises biotin.

23.   A method according to any of claims 15-22, wherein the lysine reactive agent comprises a hindered Michael reagent.

24.   A method according to claim 23, wherein the hindered Michael agent comprises a compound having the following structure:
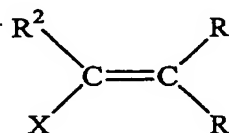
$$R^2 \diagdown \atop X \diagup C = C \diagup R \atop \diagdown R$$

wherein X is an electron withdrawing group that is capable of stabilising a negative charge; the R groups independently comprise a hydrogen, a halogen, an alkyl, an aryl, or an aromatic group with the proviso that at least one of the R groups comprises a sterically hindering group; and the group R^2 comprises a hydrogen, a halogen, a hydrocarbon

group, an electron withdrawing group and/or a linker capable of attachment to an affinity capture functionality or a solid phase support.

25.   A labelled analyte compound, which compound has the following structure:

<p style="text-align:center">D-M-L-A</p>

wherein D comprises a light absorbing label, M comprises a mass modifier, L comprises a linker and A comprises an analyte.

26.   A compound according to claim 25, wherein D comprises a non-fluorescent dye.

27.   A compound according to claim 26, wherein D comprises a cinnamic acid derivative, a nicotinic acid derivative, a picolinic acid derivative, a hydroxybenzoic acid derivative, a methoxybenzoic acid derivative or a sinapinic acid derivative.

28.   A compound according to claim 26 or claim 27, wherein the non-fluorescent dye comprises a compound selected from 4-dimethylaminoazobenzine-4'-sulphonyl chloride (DABSYL chloride), 3-hydroxypicolinic acid, 2,5-dihydroxybenzoic acid and 4-hydroxy-alpha-cyanocinnamic acid.

29.   A compound according to any of claims 25-28, wherein M is selected from a compound formed from an aryl ether, and an oligomer formed from 2 or more aryl ether units.

30.   A compound according to any of claims 25-28, wherein the linker comprises a group selected from $-CR_2-CH_2-SO_2-$, $-N(CR_2-CH_2-SO_2-)_2$, $-NH-CR_2-CH_2-SO_2-$, -CO-NH-, -CO-O-, -NH-CO-NH-, -NH-CS-NH-, -CH2-NH-, -SO2-NH-, -NH-CH2-CH2- and -OP(=O)(O)O-.

31.   A compound according to any of claims 25-30, wherein A is selected from a protein, a polypeptide, a peptide, a peptide fragment and an amino acid.

32.   A compound for labelling an analyte, which compound has the following structure:

M-L-R

wherein M is a mass marker comprising a cinnamic acid derivative, a nicotinic acid derivative, a picolinic acid derivative, a hydroxybenzoic acid derivative, a methoxybenzoic acid derivative or a sinapinic acid derivative, L comprises a linker and R comprises a reactive functionality for attaching the compound to an analyte.

33.   A compound according to claim 32, wherein M comprises a non-fluorescent dye compound selected from 4-dimethylaminoazobenzine-4'-sulphonyl chloride (DABSYL chloride), 3-hydroxypicolinic acid, 2,5-dihydroxybenzoic acid and 4-hydroxy-alpha-cyanocinnamic acid.

34.   A compound according to claim 32 or claim 33, wherein M further comprises a compound formed from an aryl ether, or an oligomer formed from 2 or more aryl ether units.

35.   A compound according to any of claims 32-34, wherein the linker comprises a group selected from $-CR_2-CH_2-SO_2-$, $-N(CR_2-CH_2-SO_2-)_2$, $-NH-CR_2-CH_2-SO_2-$, -CO-NH-, -CO-O-, -NH-CO-NH-, -NH-CS-NH-, -CH2-NH-, -SO2-NH-, -NH-CH2-CH2-, -OP(=O)(O)O- and an amide linkage through the acid groups of M.

36.   A compound according to any of claims 32-35, wherein R is for attaching the compound to a protein, a polypeptide, a peptide, a peptide fragment or an amino acid.

37.   A compound according to any of claims 32-36, wherein R comprises an ester group, an acid anhydride group, an acid halide group such as an acid chloride,, an N-hydroxysuccinamide group, a pentafluorophenyl ester group, a maleimide group, an alkenyl sulphone group, or an iodoacetamide group.

38.   A compound according to any of claims 25-37, which compound further comprises an affinity ligand.

39.   A compound according to claim 38, wherein the affinity ligand comprises biotin.

40.   A compound according to any of claims 25-39, which compound further comprises an ionisable moiety.

41.   A compound according to claim 40, wherein the ionisable moiety is selected from a tertiary amino group, a guanidino group and a sulphonic acid group.

42.   A compound according to any of claims 25-41, which compound comprises a cinnamic acid functionality.

43.   An array of two or more compounds for labelling an analyte, wherein the compounds in the array are compounds as defined in any of claims 32-42 and wherein each compound in the array differs in mass from all other compounds in the array.

44.   An array of compounds according to claim 43, wherein the difference in mass of each of the compounds in the array is achieved by isotopic substitution.

45.   A kit for characterising an analyte by matrix assisted laser desorption ionisation (MALDI) mass spectrometry, which kit comprises:

    (a)   one or more light absorbing labels having a reactive functionality for attaching the labels to an analyte; and

(b)   a compound for forming a matrix, which compound absorbs light at the
same frequency as the light-absorbing label.

46.   A kit according to claim 45, wherein the component (a) comprises a compound, or
an array of compounds, as defined in any of claims 32-44.

47.   A kit for characterising an analyte by matrix assisted laser desorption ionisation
(MALDI) mass spectrometry, which kit comprises:

(a)   a compound, or an array of compounds, as defined in any of claims 32-44;

(b)   an ion exchange resin.

48.   A kit according to claim 47, wherein the compound or array of compounds
comprises an ionisable moiety that forms a positive charge, and wherein the ion exchange
resin comprises a cation exchange resin.

49.   A kit according to claim 47, wherein the compound or array of compounds
comprises an ionisable moiety that forms a negative charge, and wherein the ion
exchange resin comprises a anion exchange resin.

Fig.1.

Synthesis of 2-Cyan-3-(4-tert-butoxycarbonyloxyphenyl) acrylic acid-N-(hydroxysuccinimidester) [NHS-HCCA]:

189,2

__1__

289,3

__2__

386,4

__3__
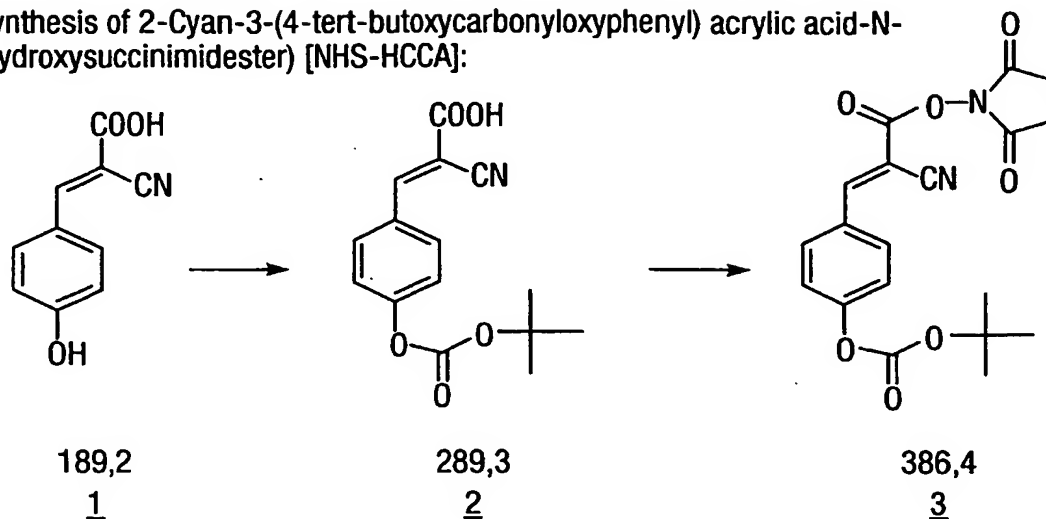
Synthesis of 2-Cyan-3-(4-tert-hydroxyphenyl) acrylic acid-6-[(2,5-dioxo-1-pyrrolidinyl) oxy)-(6-oxo) hexyl] amide [NHS-L-HCCA]:

131

207.7

__1__

198.3

__2__

198.3

__2__

122.1

302.3

__3__

__3__

115.1

399.4   __4__

2/22

Fig.2.

NH-HRDPYRFDPHKD–OH : Peptide+MT

NH₂-HRDPYRFDPHKD–OH : Peptide

Fig.3.

NH-HRDPYRFDPHKD-OH : Peptide+MT

NH₂-HRDPYRFDPHKD-OH : Peptide

[Peptide+H]⁺ +MT

[Peptide+H]⁺

2021.0

1849.9

1754.8

1738.4

1582.7

1519.6
1511.5

1397.5
1395.4

1277.3

1175.3
1162.3

1106.2

m/z

Intensity

Fig.4.

NH₂-HSRGHRGHSHAHRG-OH : A (m/z = 1522.75)
NH-HSRGHRGHSHAHRG-OH : B (m/z = 1806,87)

50%/50% of Peptides A and B.
Conc = 1µmol/µl
0.5µl on the Maldi target

Fig.5a.

^{1}NH$_2$-DEGPYKMEHFRWGSPPKD-CO$_2$H

$\longrightarrow$

^{1}NH$_2$DEGPYK-CO$_2$H

^{7}NH$_2$-MEHFR-CO$_2$H

^{12}NH$_2$-WGSPPKD-CO$_2$H

Matrix MT labelling $\longrightarrow$

^{6}SMT

SMT-^{1}NH$_2$-DEGPYK-CO$_2$H

SMT-^{7}NH$_2$-MEHFR-CO$_2$H

SMT-^{12}NH$_2$-WGSPPKD-CO$_2$H

^{18}SMT

Fig.5b.

Maldi MS of β-MSH   [MH]+=2175,98

655.9644

2175.7440

2197.7156

2219.6898

2241.7008

m/z

Intensity

100

0

1000   3000

Fig.6.

Expected cleavage masses
of the tryptic digest of β-MSH

	m/z (mi)	m/z (av)	Cleavages		Sequence
✓	708.3204	708.7507	1	6	(-) DEGPYK (M)
✓	719.3299	719.8458	7	11	(K) MEHFR (W)
✓	786.3786	786.8682	12	18	(R) WGSPPKD (-)

Peaks labelled (top spectrum):
1434.6496
1408.6362
842.5148 (Trypsin)
808.3604
786.3762 (12-18) Na
763.3012
741.2977 Na
719.3291 (7-11) Na
708.3061 (1-6)

m/z axis: 700 · 1000 · 1300 · 1600
Intensity (y-axis), 0

Expected cleavage masses
of SMT labelling of the tryptic digest

	m/z (mi)	Cleavages		Sequence
	992.435	1	6	(-) DEGPYK (M) + 1SMT
✓	1276.535	1	6	(-) DEGPYK (M) + 2SMT
✓	1003.445	7	11	(K) MEHFR (W) + 1SMT
✓	1287.560	7	11	(K) MEHFR (W) + 2SMT
✓	1354.609	12	18	(R) WGSPPKD (-) + 2SMT

Peaks labelled (bottom spectrum):
1398.4646
1376.4368 (12-18+2 SMT+Na) Na
1342.4348
1320.4102
1298.4302 (1-6+2 SMT+Na) Na
1287.4408 (7-11+2 SMT)
1069.3003
1047.3031 Na
1025.3143 Na
1003.3409 (7-11+1 SMT) Na

m/z axis: 700 · 1000 · 1300 · 1600
Intensity (y-axis), 0

Fig.7.

ratio 95% / 5%
non labelled (m/z= 719) /
labelled (m/z= 1003)

Intensity

568.1616
609.2846
768.3495
719.3709
741.3568
786.4285
808.4093
842.5582
1003.4936
1019.5010
1025.4886
1067.4271
1126.7496
1192.5574
1287.6889
1298.6496
1376.6748
1434.7265
1484.2790

m/z

600   1600

---

ratio 50% / 50%
non labelled (m/z= 719) / labelled (m/z= 1003)

Intensity

719.3787
1003.4954
1287.6288
1298.6164
1376.6671

m/z

600   1600

---

ratio 5% / 95%
non labelled (m/z= 719) / labelled (m/z= 1003)

Intensity

X
1003.4450
1120.0745
1287.5535
1298.5117
1376.5757

m/z

600   1600

Fig.8.

Fig.8 (Cont).

Original tryptic peptide mixture concentration:
20% (labelled=0,1 µg/µl) as B/80% (not labelled=0,4µg/µl) as A
1µl of the mixture was used for Maldi MS

Ratio 80% mixture A/20% mixture B
non labelled (m/z=719)/labelled (m/z=1003)

Dilution=3125x
~14fmol (B)/58fmol (A)

1003.5269

Dilution=15625x
~3fmol (A)/12 fmol (B)

1003.4674

m/z

Intensity

X

Fig.9.

1-Tryptic peptide mixture of BSA

842.4595
877.0170
927.4680
949.4629
970.4790
1022.4129
1050.4218
1146.5788
1163.6069
1185.5998
1249.6052
1283.6973
1305.6960
1327.6770
1416.7126
1423.3331
1439.8041
1461.7786
1479.7880
1501.7622
1522.7636
1522.7939
1567.7394
1589.7173
1610.7709
1631.6236
1639.9368
1667.8214
1682.9631
1788.8329
1823.9162
1888.9371
1910.9045
1940.8059
2045.0368
2067.0373
2314.1279
2506.2639
2587.1190

Intensity
100

0

1000   m/z   2600

Fig.10.

15/42 matches (35%). 69293.9 Da, pI=5.82. Acc. # swiss:P02769. BOVIN. SERUM ALBUMIN PRECURSOR..

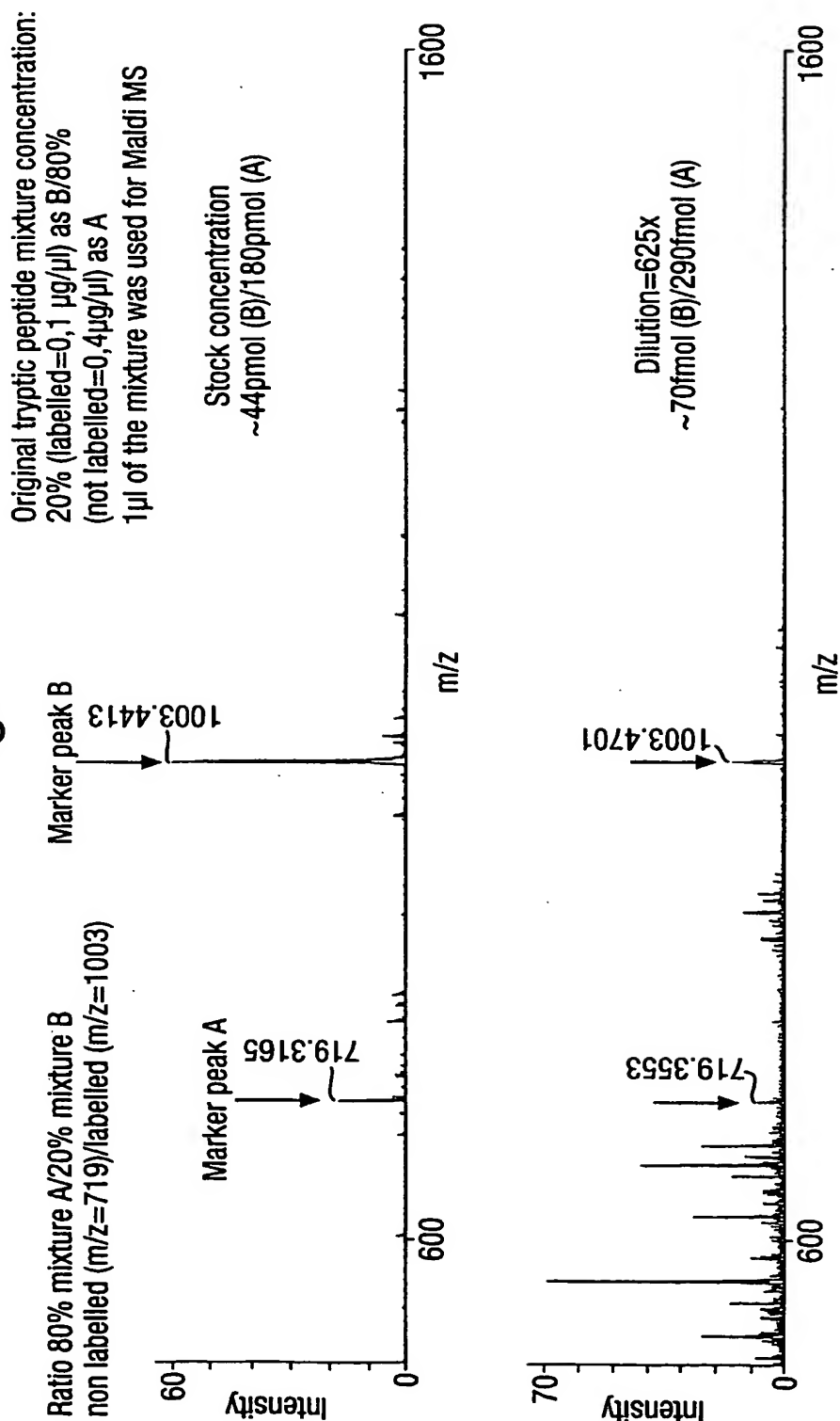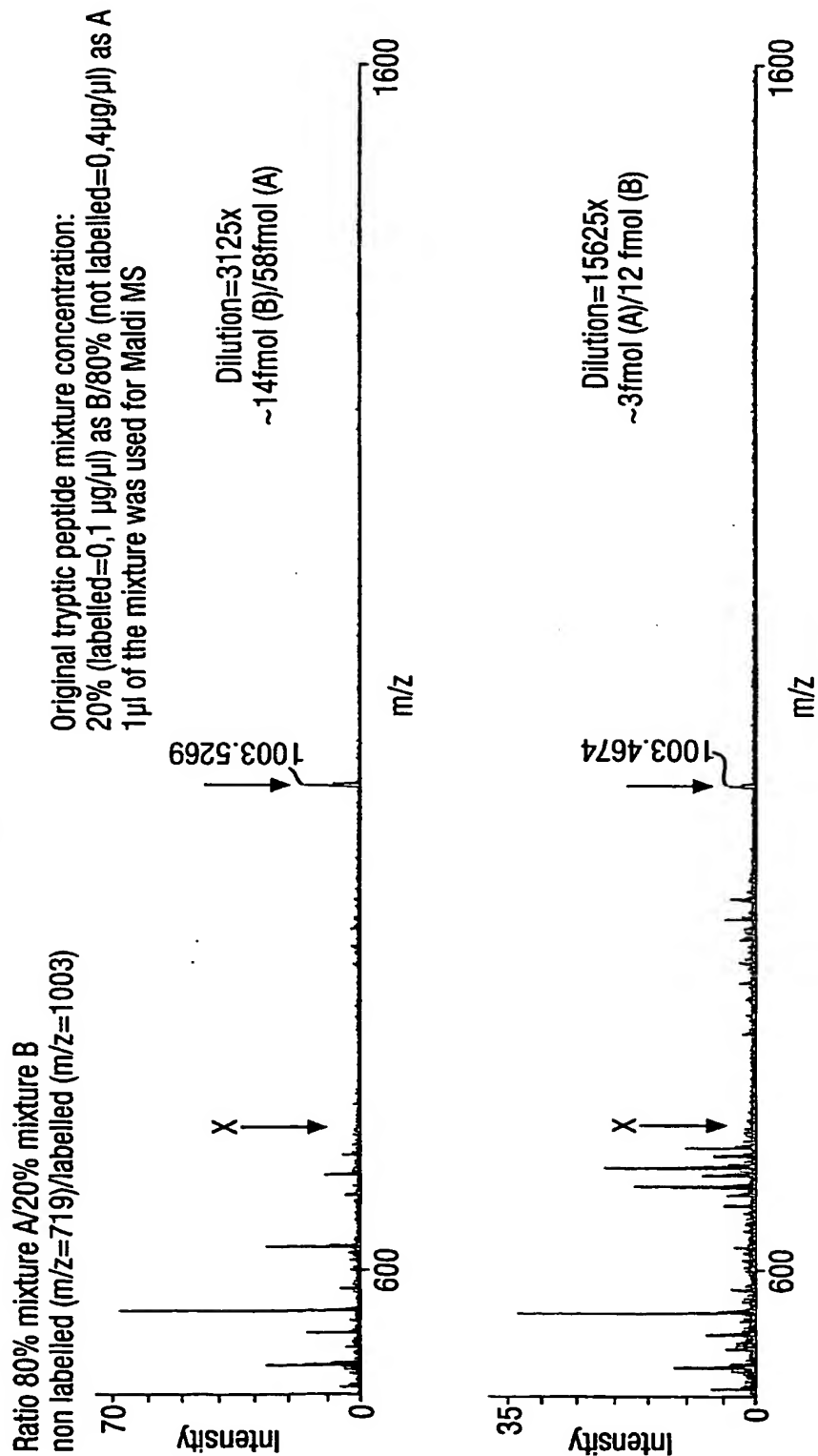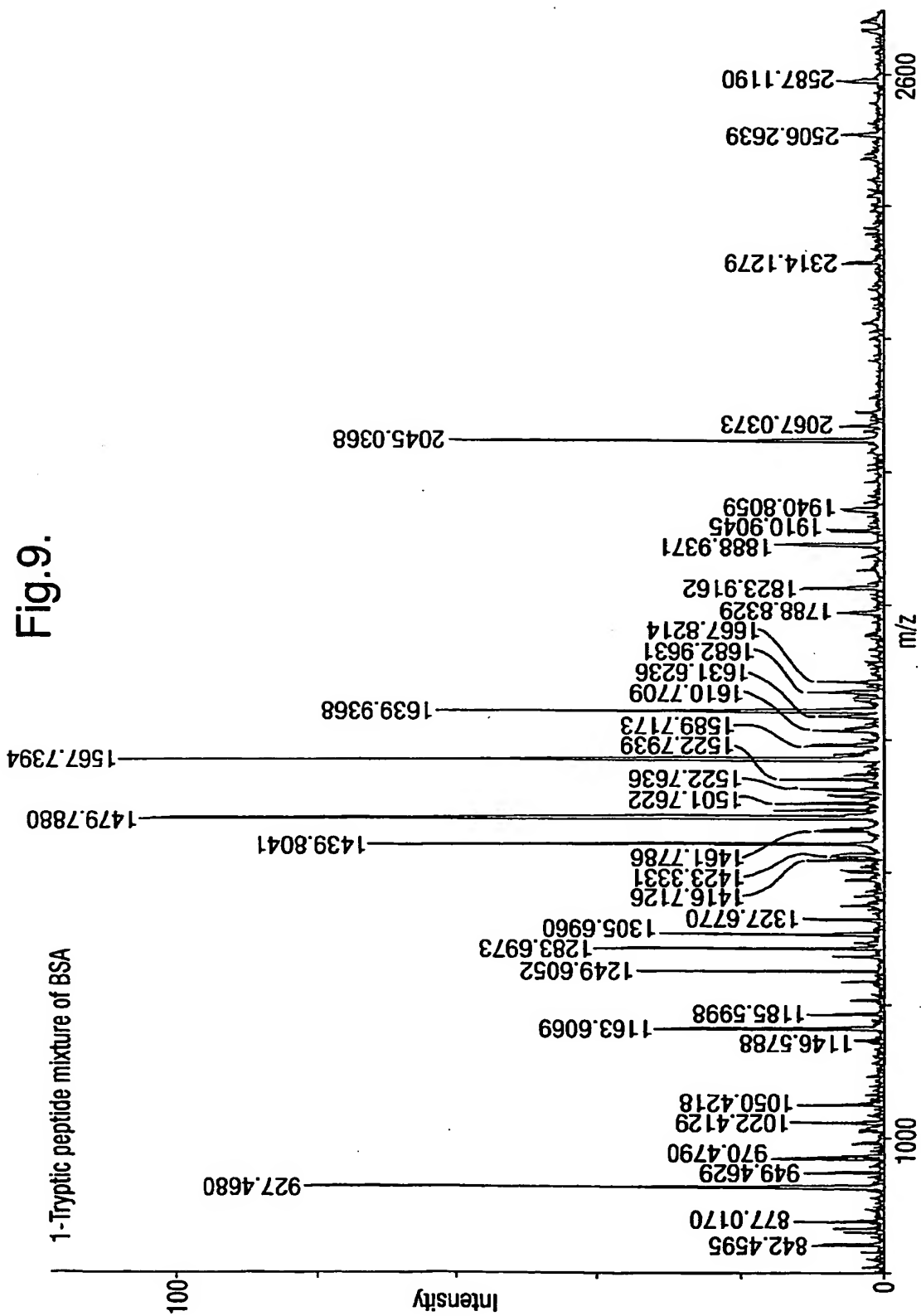| m/z submitted	MH+ matched	Δppm	start	end	Peptide Sequence	Modifications
927.4680	927.4940	-28.0249	161	167	(K)LYEIAR (R)	
1163.6069	1163.6312	-20.8956	66	75	(K)LVNELTEFAK (T)	
1249.6052	1249.6217	-13.2142	35	44	(R)FKDLGEEHFK (G)	
1283.69713	1283.7112	-10.8252	361	371	(R)HPEYAVSVLLR (L)	
1305.6960	1305.7167	-15.8348	402	412	(K)HLVDEPQNLIK (Q)	
1439.8041	1439.8123	-5.7004	360	371	(R)RHPEYAVSVLLR (L)	
1479.7880	1479.7960	-5.3985	421	433	(K)LGEYGFQNALIVR (Y)	
1567.7394	1567.7433	-2.4778	347	359	(K)DAFLGSFLYEYSR (R)	
1639.9368	1639.9383	-0.9122	437	451	(R)KVPQVSTPTLVEVSR (S)	
1667.8214	1667.8137	4.6234	469	482	(R)MPCTEDYLSLILNR (L)	
1823.9162	1823.9002	8.7746	508	523	(R)RPCFSALTPDETYVPK (A)	
1888.9371	1888.9274	5.1368	169	183	(R)HPYFYAPELLYYANK (Y)	
2045.0368	2045.0285	4.0547	168	183	(R)RHPYFYAPELLYYANK (Y)	
2506.2639	2506.2508	5.2276	469	489	(R)MPCTEDYLSLILNRLCVLHEK (T)	
3395.6670	3395.6438	6.8340	558	587	(K)HKPKATEEQLKTVMENFVAFVDKCCAADDK (E)	1Met-ox

The matched peptides cover 28% (174/607 AA's) of the protein
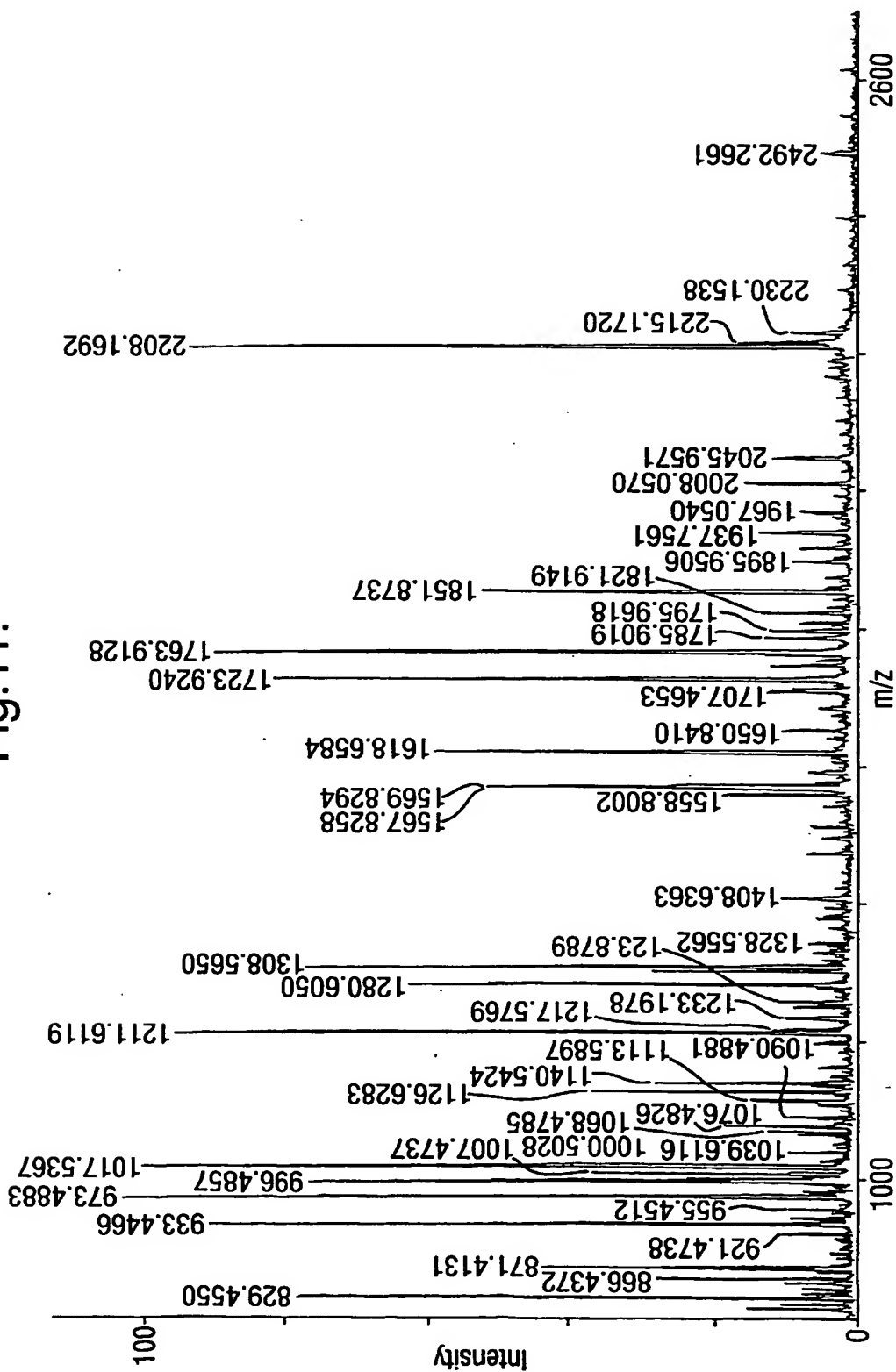
Fig.11.

Fig.12.

16/50 matches (32%). 69293.9 Da, pI = 5.82. Acc. # swiss: P02769. BOVIN. SERUM ALBUMIN PRECURSOR.

m/z submitted	MH+ matched	Δ ppm	start	end	Peptide Sequence	Modifications
829.4550	829.4572	-2.6686	101	105	(K) VASLR (E)	1SMT
933.4466	933.4504	-4.0854	205	209	(K) IETMR (E)	1SMT
933.4466	933.4504	-4.0854	223	228	(R) CASIQK (F)	1SMT
973.4883	973.4896	-1.3110	236	241	(K) AWSVAR (L)	1SMT
996.4857	996.4903	-4.6207	29	34	(K) SEIAHR (F)	1SMT
1068.4785	1068.4791	-0.5345	25	28	(R) DTHK (S)	1SMT
1211.6119	1211.6101	1.4977	161	167	(K) YLYEIAR (R)	1SMT
1217.5769	1217.5665	8.5367	223	228	(R) CASIQK (F)	2SMT
1233.5978	1233.6097	-9.6395	156	160	(K)KFWGK (Y)	2SMT
1308.5650	1308.5717	-5.0955	499	507	(K) CCTESLVNR (R)	1SMT
1567.8258	1567.8273	-0.9497	361	371	(R) HPEYAVSVLLR (L)	1SMT
1569.8294	1569.8218	4.8352	233	241	(R) ALKAWSVAR (L)	2SMT
1723.9240	1723.9284	-2.5523	360	371	(R) RHPEYAVSVLLR (L)	1SMT
1763.9128	1763.9121	0.4075	421	433	(K) LGEYGFQNALIVR (Y)	1SMT
1795.9618	1795.9594	1.3222	438	451	(K) VPQVSTPTLVEVSR (S)	1SMT
1851.8737	1851.8594	7.7344	347	359	(K) DAFLGSFLYEYSR (R)	1SMT
2208.1692	2208.1705	-0.5801	437	451	(R) KVPQVSTPTLVEVSR (S)	2SMT

The matched peptides cover 17% (109/607 AA's) of the protein

14/22

Fig.13.

Fig.14.

7/56 matches (12%). 35691.1 Da, pI=8.52. Acc. # swiss:P46406. RABIT. GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) (GAPDH)..

m/z submitted	MH⁺ matched	Δppm	start	end	Peptide Sequence	Modifications
977.5324	977.5420	-9.8265	70	77	(K)AITIFQER (D)	
1499.7853	1499.7892	-2.5929	232	245	(R)VPTPNVSVVDLTCR (L)	
1615.8755	1615.8808	-3.2682	70	83	(K)AITIFQERDPANIK (W)	
1763.8175	1763.8029	8.2636	307	320	(K)LISWYDNEFGYSNR (V)	
2618.3883	2618.3765	4.5189	160	183	(K)VIHDHFGIVEGLMTTVHAITATQK (T)	
3317.5310	3317.5651	-10.2886	25	52	(K)VDVVAINDPFIDLHYMVYMFQYDSTHGK (F)	
3339.6063	3339.6432	-11.0492	84	115	(K)WGDAGAEYVVESTGVFTTMEKAGAHLKGGAKR (V)	1Met-ox

The matched peptides cover 37% (126/332 AA's) of the protein
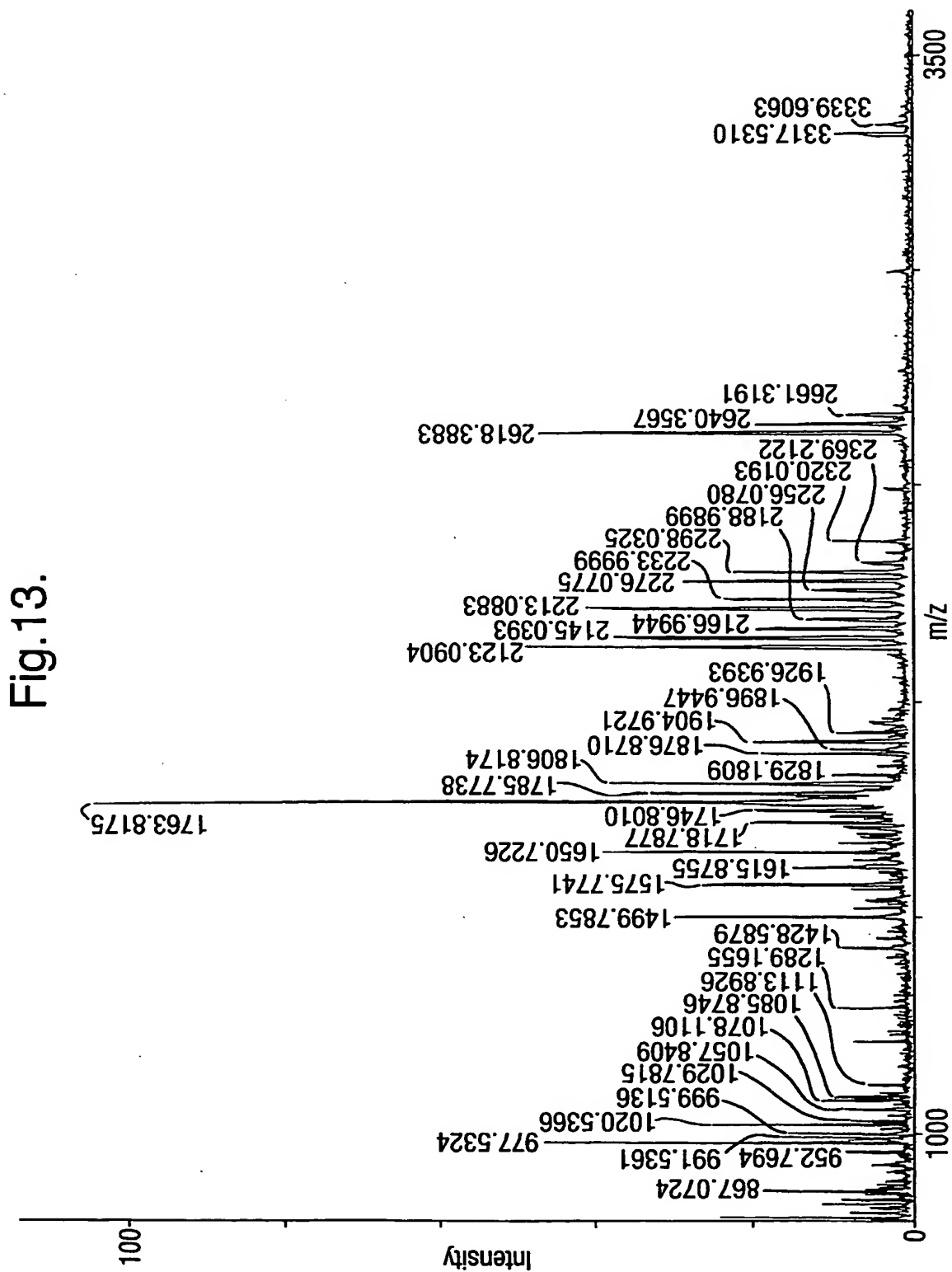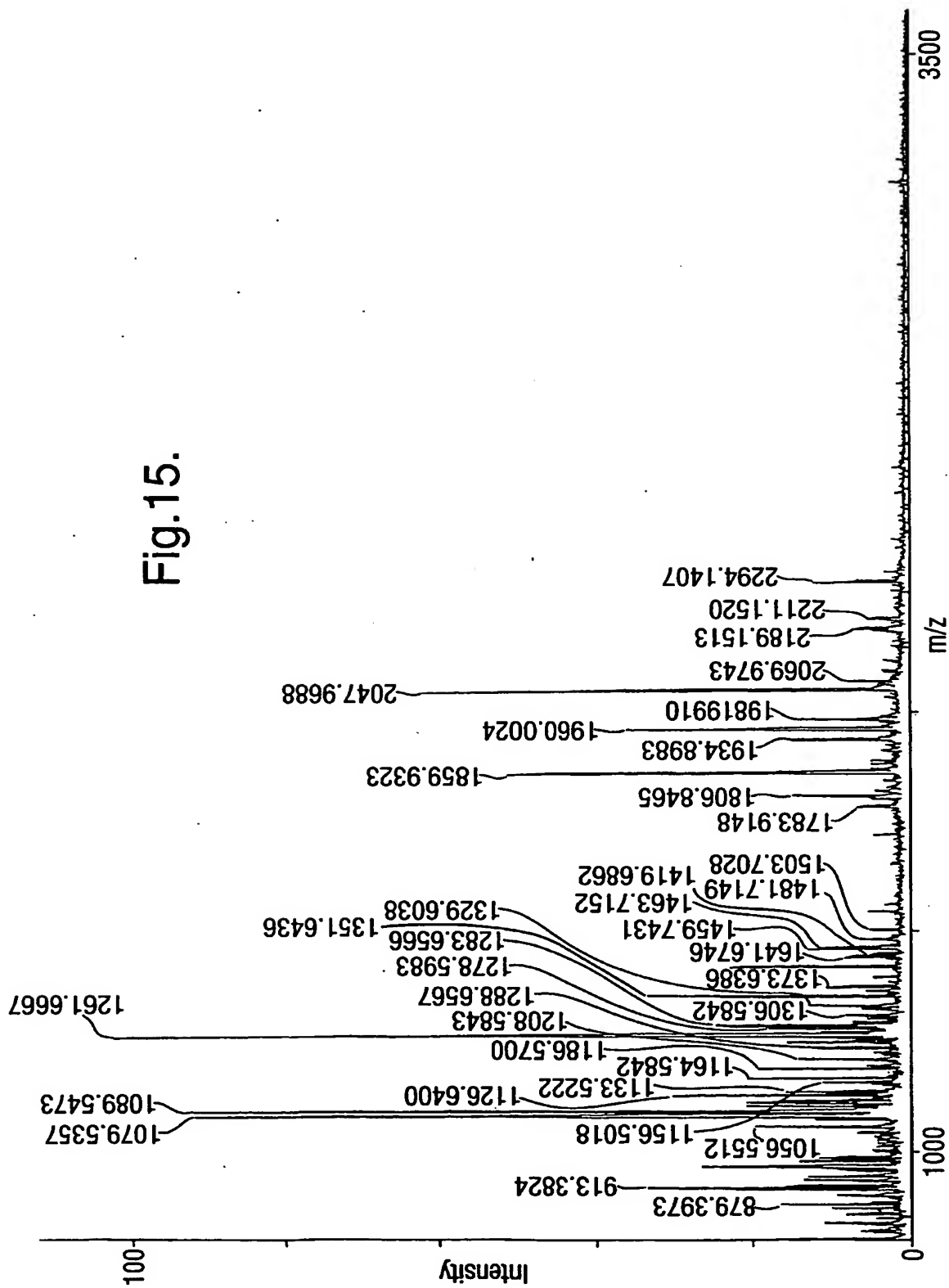
Fig.15.

Fig.16.

9/52 matches (17%). 35691.1 Da, pI=8.52. Acc. # swiss:P46406. RABIT. GLYCERALDEHYDE
3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) (GAPDH)..

m/z submitted	MH+ matched	Δppm	start	end	Peptide Sequence	Modifications
1056.5512	1056.5267	23.1986	111	115	(K)GGAKR(V)	2SMT
1079.5357	1079.5348	0.8227	225	231	(K)LTGMAFR (V)	1SMT
1089.54473	1089.5482	-0.7836	3	10	(K)VGVNGFGR (I)	1SMT
1164.5842	1164.5842	-0.0042	105	110	(K)AGAHLK(G)	2SMT
1261.6667	1261.6581	6.8178	70	77	(K)AITIFQER (D)	1SMT
1783.9148	1783.8808	19.0702	184	194	(K)TVDGPSGKLWR(D)	2SMT
1783.9148	1783.9053	5.3359	232	245	(R)VPTPNVSVVDLTCR (L)	1SMT
1960.0024	1959.9897	6.4986	252	260	(K)YDDIKKVVK(Q)	3SMT
1981.9910	1982.0096	-9.3660	195	212	(R)DGRGAAQNIIPASTGAAK (A)	1SMT
2047.9688	2047.9190	24.3090	307	320	(K)LISWYDNEFGYSNR (V)	1SMT

The matched peptides cover 30% (100/332 AA's) of the protein

Fig.17a.

Fig.17b.

Fig.17c.

Fig.17d.

Fig.18.

(a) Cl-CH2-COCl, TEA, CH2Cl2; (b) KCN, K2CO3, H2O; (c) NC-CH2-CO2Su, NaHCO3, THF/H2O; (d) conc. H2SO4; (e) 7, Pyridine, [Piperidine]-HO-Su, DCC, Acetonitrile

Fig.19.

(a) EDTA·4Na·H₂O, NaHCO₃, NC-CH₂-CO₂Su, H₂O/Acetone;
(b) HO-C₆H₄-CHO, Pyridine, [Piperidine]; (c) HO-Su, DCC, CH₂Cl₂

Fig.20.

(a) HO-Su, DCC, CH$_2$Cl$_2$, 6-Amino-hexanoic acid; (b) HO-Su, DCC, CH$_2$Cl$_2$

Fig.21.
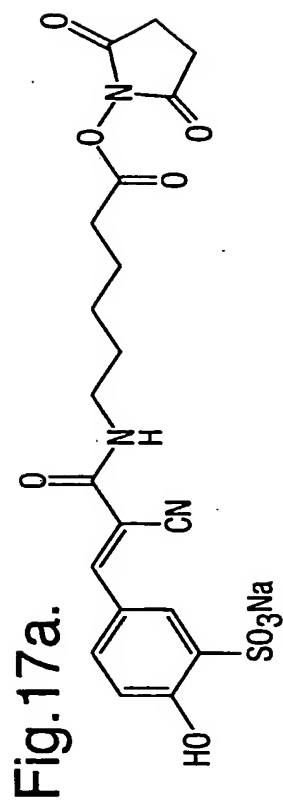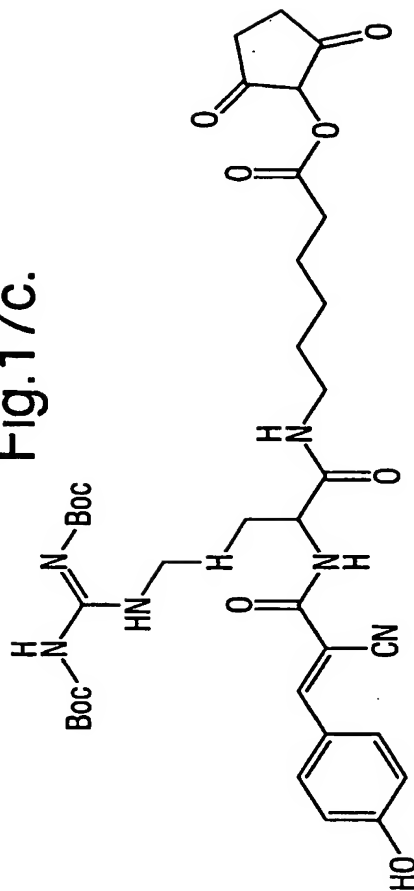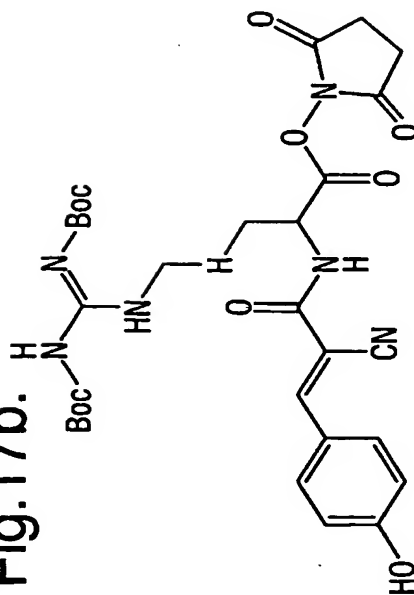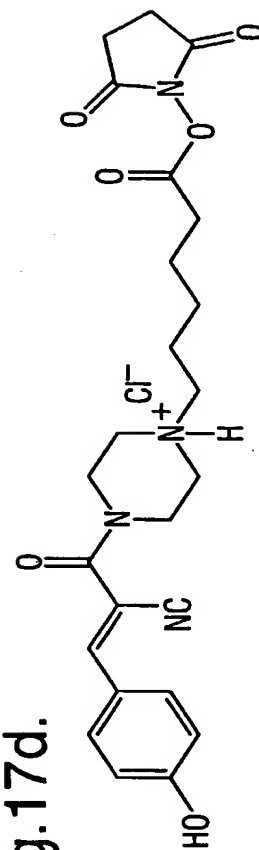
(a) l-(CH2)5-CO2Et, (isopropyl)2EtN, THF; (b) 2N HCl; (c) Cl-CH2-COCl, TEA, CH2Cl2; (d) KCN, DMSO;
(e) 4-HO-C6H4-CHO, Pyridine, [Piperidine]; (f) 2N-NaOH/CH3OH; 2N-HC1; (g) HO-Su, DCC,DMF

INTERNATIONAL SEARCH REPORT

PCT/GB 03/01485

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7   G01N33/68   C12Q1/68   C07K1/13

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7   G01N   C12Q   C07K
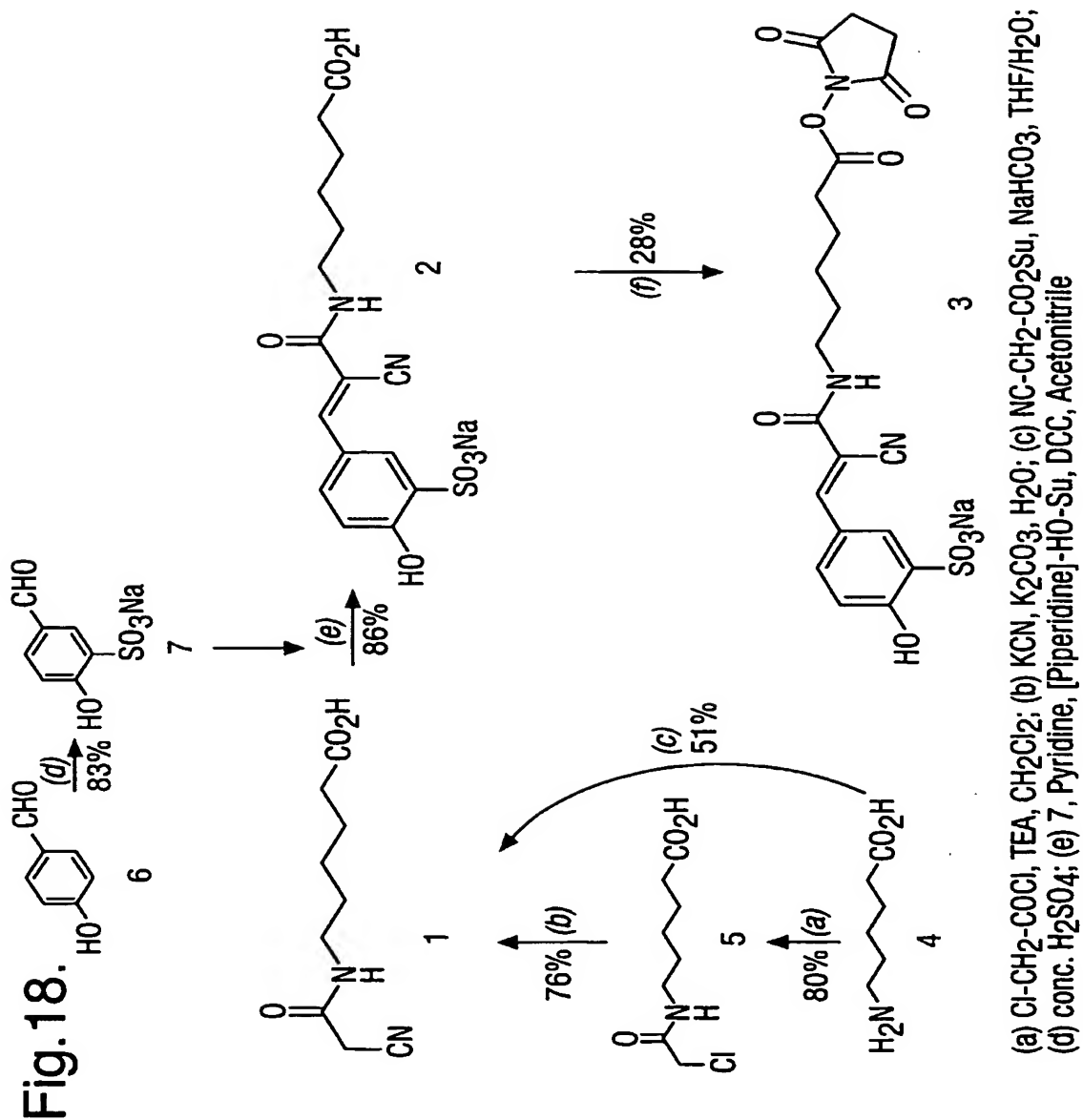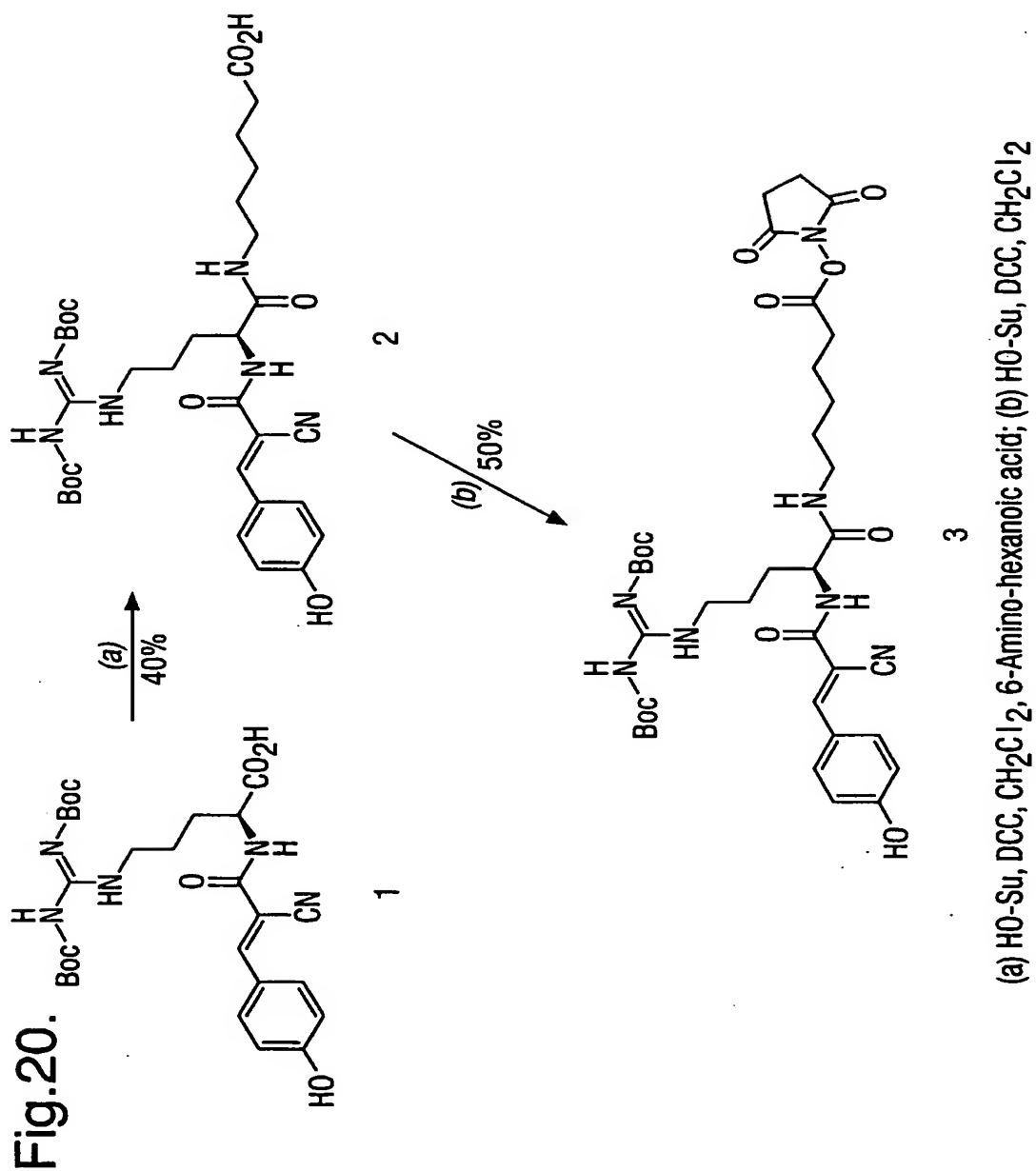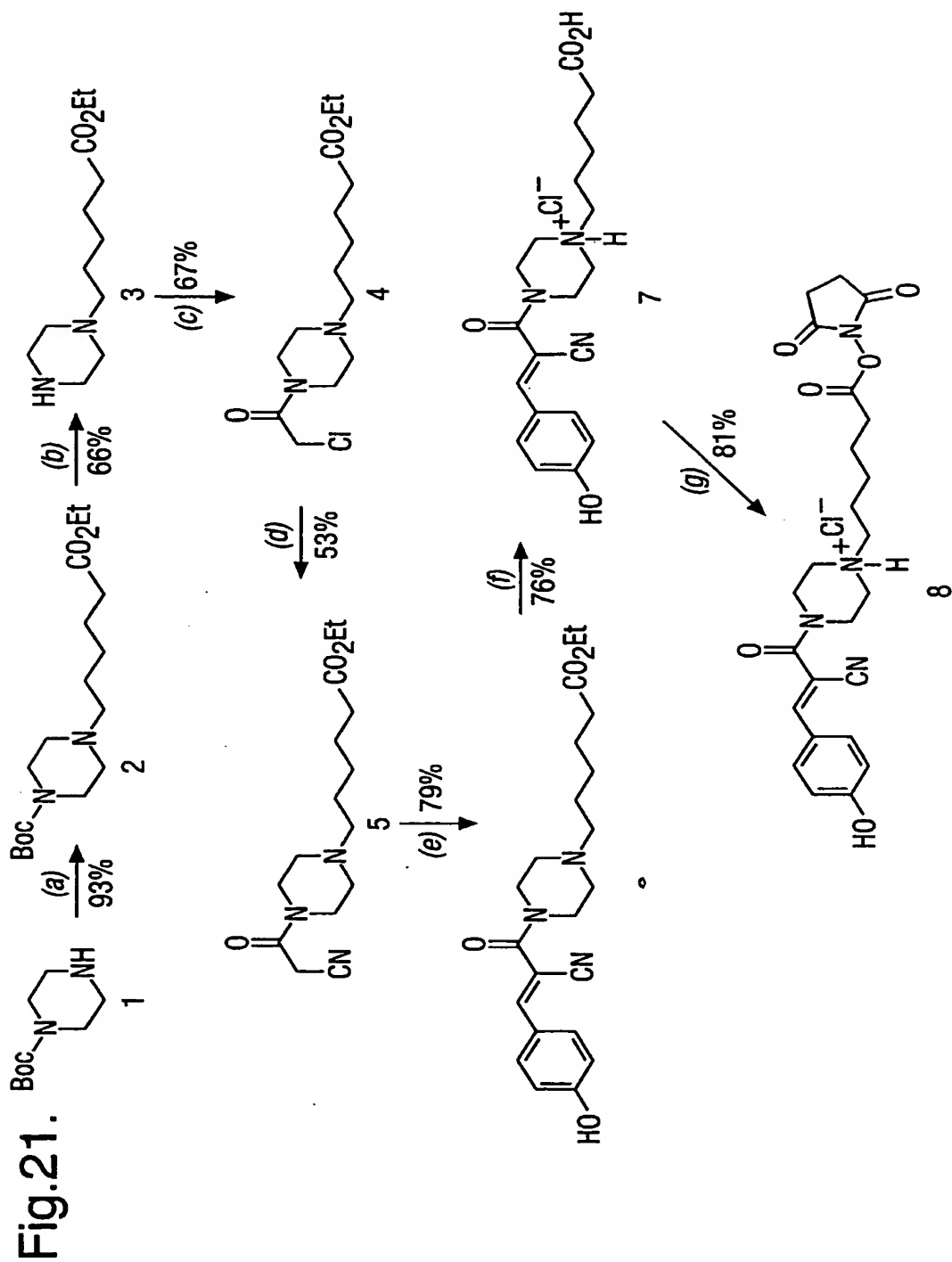
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 31830 A (BRAX GENOMICS LTD ;THOMPSON ANDREW HUGIN (GB); SCHMIDT GUENTER (GB) 23 July 1998 (1998-07-23) page 2 -page 4 page 11 -page 12 page 17 -page 18 page 27 -page 28 page 34 -page 36 page 41 -page 43; figures 5-7 -/--	1,3,4, 7-10,45

| [X] Further documents are listed in the continuation of box C. | [X] Patent family members are listed in annex. |

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
18 August 2003	02/09/2003

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Diez Schlereth, D

Form PCT/ISA/210 (second sheet) (July 1992)

page 1 of 3

INTERNATIONAL SEARCH REPORT

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01 68664 A (THOMPSON ANDREW HUGIN ;BRAX GROUP LTD (GB); SCHMIDT GUNTER (GB); J) 20 September 2001 (2001-09-20) page 4, paragraph 4 -page 4, paragraph 5 page 9 -page 16 page 22 -page 24 page 32 page 64 -page 69; figures 6,10	1,3,4,7, 9,14,25, 26, 29-31, 38,39,45
Y		15-24, 27,28, 32-44, 47-49

Y	WO 00 20870 A (THOMPSON ANDREW HUGIN ;BRAX GROUP LTD (GB); SCHMIDT GUENTER (GB)) 13 April 2000 (2000-04-13) page 5 -page 8 page 14 -page 15	15-24

P,X	WO 02 29003 A (UNIV COLUMBIA) 11 April 2002 (2002-04-11) page 26, line 4 -page 28, line 15 page 37 page 56, line 9 -page 58, line 20; figures 3,4,7	32, 35-37,43

Y	PATENT ABSTRACTS OF JAPAN vol. 017, no. 506 (C-1110), 13 September 1993 (1993-09-13) & JP 05 137599 A (TAKARA SHUZO CO LTD), 1 June 1993 (1993-06-01) abstract	27,28, 32-44

Y	US 5 708 137 A (TOTH MIHALY V ET AL) 13 January 1998 (1998-01-13) abstract; example 1	27,28, 32-44

A	M. MÜNCHBACH ET AL: "Quantitation and facilitated de novo sequencing of proteins by isotopic N-terminal labeling of peptides with a fragmentation-directing moiety" ANALYTICAL CHEMISTRY, vol. 72, 2000 - 8 March 2000 (2000-03-08), pages 4047-4057, XP002208695 the whole document	25-37, 43-46

A	WO 99 60007 A (HAMILTON ALAN LEWIS ;SHCHEPINOV MIKHAIL SERGEEVICH (GB); SOUTHERN) 25 November 1999 (1999-11-25) page 40	25-37, 43-46

-/—

1

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
A	WO 02 12893 A (MASSACHUSETTS INST TECHNOLOGY) 14 February 2002 (2002-02-14) page 14 -page 16 ---	25-37, 43-46
A	US 5 986 076 A (OLEJNIK JERZY ET AL) 16 November 1999 (1999-11-16) figures 1-21 ---	25-37, 43-46
Y	WEINBERGER S R ET AL: "RECENT TRENDS IN PROTEIN BIOCHIP TECHNOLOGY" PHARMACOGENOMICS, ASHLEY PUBLICATIONS, GB, vol. 1, no. 3, November 2000 (2000-11), pages 395-416, XP009009627 ISSN: 1462-2416 cited in the application the whole document -----	47-49

INTERNATIONAL SEARCH REPORT

PCT/GB 03/01485

Box I   Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
   because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.:   25-49(partially)
   because they relate to parts of the International Application that do not comply with the prescribed requirements to such
   an extent that no meaningful International Search can be carried out, specifically:
   see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II   Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all
   searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment
   of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report
   covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is
   restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest   ☐ The additional search fees were accompanied by the applicant's protest.

                               ☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet (1)) (July 1998)

FURTHER INFORMATION CONTINUED FROM   PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 25-49(partially)

Present claims 25-49 relate to an extremely large number of possible
compounds/arrays/kits. Support within the meaning of Article 6 PCT and/or
disclosure within the meaning of Article 5 PCT is to be found, however,
for only a very small proportion of the compounds/arrays/kits claimed. In
the present case, the claims so lack support, and the application so
lacks disclosure, that a meaningful search over the whole of the claimed
scope is impossible. Consequently, the search has been carried out for
those parts of the claims which appear to be supported and disclosed,
namely those parts relating to compounds (and arrays and kits comprising
said compounds) comprising (1) photocleveable mass tags as labels for
detection of polypeptides/nucleic acids by mass spectrometry, and (ii)
peptides labeled with DABSYL.

The applicant's attention is drawn to the fact that claims, or parts of
claims, relating to inventions in respect of which no international
search report has been established need not be the subject of an
international preliminary examination (Rule 66.1(e) PCT). The applicant
is advised that the EPO policy when acting as an International
Preliminary Examining Authority is normally not to carry out a
preliminary examination on matter which has not been searched. This is
the case irrespective of whether or not the claims are amended following
receipt of the search report or during any Chapter II procedure.

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 9831830	A	23-07-1998	AU	725966 B2	26-10-2000
			AU	5570098 A	07-08-1998
			CN	1250483 T	12-04-2000
			EP	0979305 A1	16-02-2000
			WO	9831830 A1	23-07-1998
			JP	2001508307 T	26-06-2001
			NZ	336769 A	26-01-2001
			AT	237626 T	15-05-2003
			AU	1770499 A	12-07-1999
			DE	69813622 D1	22-05-2003
			EP	1042345 A1	11-10-2000
			WO	9932501 A1	01-07-1999
			US	6287780 B1	11-09-2001
WO 0168664	A	20-09-2001	AU	4083401 A	24-09-2001
			CA	2403114 A1	20-09-2001
			CN	1427953 T	02-07-2003
			EP	1275004 A2	15-01-2003
			WO	0168664 A2	20-09-2001
			NO	20024344 A	14-11-2002
WO 0020870	A	13-04-2000	AT	232300 T	15-02-2003
			AU	6109699 A	26-04-2000
			CA	2344642 A1	13-04-2000
			CN	1411555 T	16-04-2003
			DE	69905265 D1	13-03-2003
			DK	1117999 T3	26-05-2003
			EP	1117999 A1	25-07-2001
			WO	0020870 A1	13-04-2000
			JP	2002526778 T	20-08-2002
			NO	20011552 A	01-06-2001
			NZ	510873 A	25-10-2002
WO 0229003	A	11-04-2002	AU	9664501 A	15-04-2002
			CA	2425112 A1	11-04-2002
			WO	0229003 A2	11-04-2002
			US	2002102586 A1	01-08-2002
JP 05137599	A	01-06-1993	NONE		
US 5708137	A	13-01-1998	US	5506115 A	09-04-1996
WO 9960007	A	25-11-1999	AU	3943799 A	06-12-1999
			CA	2332862 A1	25-11-1999
			EP	1068216 A2	17-01-2001
			WO	9960007 A2	25-11-1999
			JP	2002515588 T	28-05-2002
WO 0212893	A	14-02-2002	AU	7724501 A	18-02-2002
			CA	2418105 A1	14-02-2002
			EP	1307285 A2	07-05-2003
			WO	0212893 A2	14-02-2002
			US	2002076727 A1	20-06-2002
US 5986076	A	16-11-1999	US	5643722 A	01-07-1997
			AU	2635995 A	05-12-1995
			CA	2189848 A1	23-11-1995
			JP	10500409 T	13-01-1998

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
US 5986076 A		WO	9531429 A1	23-11-1995
		US	6057096 A	02-05-2000
		US	6589736 B1	08-07-2003
		US	5948624 A	07-09-1999
		EP	0763009 A1	19-03-1997
		US	6344320 B1	05-02-2002
		US	6596481 B1	22-07-2003
		US	6358689 B1	19-03-2002
		US	5922858 A	13-07-1999
		US	2002123032 A1	05-09-2002

Form PCT/ISA/210 (patent family annex) (July 1992)